

SUBSTITUTE SEQUENCE LISTING

<110> Sumitomo Chemical Co., Ltd.

<120> TRANSFORMED CELL WITH ENHANCED SENSITIVITY TO ANTIFUNGAL COMPOUND AND USE THEREOF

<130> Q78242

<150> JP 2002/317736

<151> 2002-10-31

<160> 90

<170> PatentIn version 3.2

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<211> 1315

<212> PRT

<213> Botryotinia fuckeliana

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Ala	Leu	Leu	Glu	Lys	Gly	Arg	Glu	Val	Arg	Gln	Ser	Ala	Asn	Glu	Glu	1235	1240	1245	
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 Ala Leu Ser Ser Ile Asp Leu Pro Leu Thr Asn Val Tyr Gly Asn Lys
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 Gly Ile Arg Leu Pro Gly Ala Asp Thr Ala Glu Lys Leu Ala Leu Glu
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 Arg Glu Leu Ala Ala Leu Val Ser Arg Val Gln Arg Leu Glu Ala Arg
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 Ala Ile Thr Val Asn Asn Gln Thr Leu Pro Asp Thr Pro Asn Glu Leu
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 aaa tta agt gac gag gaa ctc gaa gca ctc cgc gaa cat gtc gac cat 432
 Lys Leu Ser Asp Glu Glu Leu Glu Ala Leu Arg Glu His Val Asp His
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Ser Asp Ile Ser Phe Ile Gln Lys Gln Leu Lys Pro Tyr Gln Gly His	
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aat gtt ttg ttt atc gac aaa gga cag act ggc cat ggc aaa gaa ata	2976
Asn Val Leu Phe Ile Asp Lys Gly Gln Thr Gly His Gly Lys Glu Ile	
980 985 990	
atc act atg ctt aca caa ctt ggt ttg gta ccc gtt gtt gtt gac tct	3024
Ile Thr Met Leu Thr Gln Leu Gly Leu Val Pro Val Val Val Asp Ser	
995 1000 1005	
gag cag cac act att ctt ctc ggc aat gga aga acc aag gag aag att	3072
Glu Gln His Thr Ile Leu Leu Gly Asn Gly Arg Thr Lys Glu Lys Ile	
1010 1015 1020	
gct tca act tat gac gtg att gtt gtg gac tca att gag tcc gct cga	3120
Ala Ser Thr Tyr Asp Val Ile Val Val Asp Ser Ile Glu Ser Ala Arg	
1025 1030 1035 1040	
aaa ctg cga tca atc gat gag ttc aag tat att cca att gtt ctc tta	3168
Lys Leu Arg Ser Ile Asp Glu Phe Lys Tyr Ile Pro Ile Val Leu Leu	
1045 1050 1055	
gct ccc gtt att cat gtc agc tta aag tct gct ttg gat ctt ggt atc	3216
Ala Pro Val Ile His Val Ser Leu Lys Ser Ala Leu Asp Leu Gly Ile	
1060 1065 1070	
act tct tac atg acc act cca tgt tta acg atc gat ctt ggc aat ggt	3264
Thr Ser Tyr Met Thr Thr Pro Cys Leu Thr Ile Asp Leu Gly Asn Gly	
1075 1080 1085	
atg att cct gct ttg gag aat cga gct gca ccc tca ttg gcg gac aac	3312
Met Ile Pro Ala Leu Glu Asn Arg Ala Ala Pro Ser Leu Ala Asp Asn	
1090 1095 1100	
aca aaa tcc ttc gac att ctc ttg gcc gaa gat aac atc gtc aat caa	3360
Thr Lys Ser Phe Asp Ile Leu Leu Ala Glu Asp Asn Ile Val Asn Gln	
1105 1110 1115 1120	

cgc tta gcg gtg aag att cta gaa aag tat cac cac gtc gtc aca gtc	3408
Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr Val	
1125 1130 1135	
ggt ggc aat ggt caa gaa gca cta gat gct atc aag gag aaa cga tac	3456
Val Gly Asn Gly Gln Glu Ala Leu Asp Ala Ile Lys Glu Lys Arg Tyr	
1140 1145 1150	
gat gtt att ctc atg gac gtt caa atg cca att atg gga gga ttc gaa	3504
Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly Gly Phe Glu	
1155 1160 1165	
gca acc gct aag att aga gag tac gaa cgg agt ctt gga acg caa aga	3552
Ala Thr Ala Lys Ile Arg Glu Tyr Glu Arg Ser Leu Gly Thr Gln Arg	
1170 1175 1180	
acg cct att atc gca ctt aca gca cac gct atg ttg ggt gat cgc gaa	3600
Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met Leu Gly Asp Arg Glu	
1185 1190 1195 1200	
aaa tgt att caa gcc caa atg gat gaa tat ctt tct aag cct ctg aaa	3648
Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Lys	
1205 1210 1215	
caa aat cat ctt att cag acg atc ttg aaa tgt gca acc ctt gga ggt	3696
Gln Asn His Leu Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly	
1220 1225 1230	
gca ttg ctc gag aag ggt agg gag gtt agg caa tcc gct aat gaa gag	3744
Ala Leu Leu Glu Lys Gly Arg Glu Val Arg Gln Ser Ala Asn Glu Glu	
1235 1240 1245	
agc ccc aat tcg caa aat ggt cct cgc ggt aca cag cat cct gca tca	3792
Ser Pro Asn Ser Gln Asn Gly Pro Arg Gly Thr Gln His Pro Ala Ser	
1250 1255 1260	
agt ccc aca cca gcc cat atg aga ccg gct atc gaa cct cgt gca tac	3840
Ser Pro Thr Pro Ala His Met Arg Pro Ala Ile Glu Pro Arg Ala Tyr	
1265 1270 1275 1280	
acg acc act ggc cct ata aat cat gga agt gca gag agt cct tca ctt	3888
Thr Thr Thr Gly Pro Ile Asn His Gly Ser Ala Glu Ser Pro Ser Leu	
1285 1290 1295	
gta acg gca gat gct gag gat cca ctt gcg agg ctt cta atg cgt gcg	3936
Val Thr Ala Asp Ala Glu Asp Pro Leu Ala Arg Leu Leu Met Arg Ala	
1300 1305 1310	
cat agc agc tag	3948
His Ser Ser	
1315	

<210> 3

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 3
 tattcagaga ctagtatgga ggattctaca atagca 36

<210> 4
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

<400> 4
 cagatgaatc tgcagctagc tgctatgcgc acg 33

<210> 5
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for sequencing

<400> 5
 gatgtactca ctggtgcccc atccccgagcc 30

<210> 6
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for sequencing

<400> 6
 ctcaaacagt tgagcatgta caccggccag 30

<210> 7'
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 <212> DNA
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<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for sequencing

<400> 7
 acagaaggta ttctcggtgg acaagccaag 30

<210> 8
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for sequencing

<400> 8
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<210> 9
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 <212> DNA
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<220>
 <223> Description of Artificial Sequence:Designed
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<400> 9
 atcttctcca acgaagtgc aagagtcgcc 30

<210> 10
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for sequencing

<400> 10
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<210> 11
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for sequencing

<400> 11
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<210> 12
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for sequencing

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<210> 13
 <211> 1315
 <212> PRT
 <213> Botryotinia fuckeliana

<400> 13
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 Ala Leu Ser Ser Ile Asp Leu Pro Leu Thr Asn Val Tyr Gly Asn Lys
 20 25 30
 Gly Ile Arg Leu Pro Gly Ala Asp Thr Ala Glu Lys Leu Ala Leu Glu
 35 40 45
 Arg Glu Leu Ala Ala Leu Val Ser Arg Val Gln Arg Leu Glu Ala Arg
 50 55 60
 Ala Ile Thr Val Asn Asn Gln Thr Leu Pro Asp Thr Pro Asn Glu Leu
 65 70 75 80
 Gly Ala Pro Ser Ala Phe Ala Asp Val Leu Thr Gly Ala Pro Ser Arg
 85 90 95
 Ala Ser Lys Ser Thr Thr Ser Arg Gln Gln Leu Val Asn Ser Leu Leu
 100 105 110
 Ala Ala Arg Glu Ala Pro Thr Gly Gly Glu Arg Pro Pro Lys Phe Thr
 115 120 125
 Lys Leu Ser Asp Glu Glu Leu Glu Ala Leu Arg Glu His Val Asp His
 130 135 140
 Gln Ser Lys Gln Leu Asp Ser Gln Lys Ser Glu Leu Ala Gly Val His
 145 150 155 160
 Ala Gln Leu Phe Glu Gln Lys Gln Arg Gln Glu Gln Ala Leu Asn Val
 165 170 175
 Leu Glu Val Glu Arg Val Ala Ala Leu Glu Arg Glu Leu Lys Lys His
 180 185 190
 Gln Gln Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Glu
 195 200 205
 Ile Val Thr Ala Val Ala Arg Gly Asp Leu Ser Lys Lys Val Gln Ile
 210 215 220
 His Ser Val Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg Val Ile
 225 230 235 240
 Asn Thr Met Met Asp Gln Leu Gln Ile Phe Ser Ser Glu Val Ser Arg
 245 250 255
 Val Ala Arg Glu Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Lys
 260 265 270
 Ile Ser Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn Val Asn
 275 280 285
 Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala Ser Val
 290 295 300
 Thr Thr Ala Val Ala His Gly Asp Leu Thr Gln Lys Ile Glu Arg Pro
 305 310 315 320
 Ala Gln Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr Met Val
 325 330 335
 Asp Gln Leu Arg Thr Phe Ala Ala Glu Val Thr Arg Val Ala Arg Asp
 340 345 350
 Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Glu Ser Glu Gly Val
 355 360 365
 Gln Gly Met Trp Asn Thr Leu Ile Val Asn Val Asn Ala Met Ala Asn
 370 375 380
 Asn Leu Thr Thr Gln Val Arg Asp Ile Ala Ile Val Thr Thr Ala Val
 385 390 395 400
 Ala Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Lys Gly Glu
 405 410 415
 Ile Lys Gln Leu Lys Glu Thr Ile Asn Ser Met Val Asp Gln Leu Gln
 420 425 430

Gln	Phe	Ala	Arg	Glu	Val	Thr	Lys	Ile	Ala	Arg	Glu	Val	Gly	Thr	Glu
		435					440					445			
Gly	Arg	Leu	Gly	Gly	Gln	Ala	Thr	Val	His	Asp	Val	Glu	Gly	Thr	Trp
		450				455					460				
Arg	Asp	Leu	Thr	Glu	Asn	Val	Asn	Gly	Met	Ala	Met	Asn	Leu	Thr	Thr
465					470					475					480
Gln	Val	Arg	Glu	Ile	Ala	Lys	Val	Thr	Thr	Ala	Val	Ala	Arg	Gly	Asp
				485						490					495
Leu	Thr	Lys	Lys	Ile	Glu	Val	Glu	Val	Gln	Gly	Glu	Ile	Ala	Ser	Leu
			500					505					510		
Lys	Asp	Thr	Ile	Asn	Thr	Met	Val	Asp	Arg	Leu	Ser	Thr	Phe	Ala	Phe
		515					520					525			
Glu	Val	Ser	Lys	Val	Ala	Arg	Glu	Val	Gly	Thr	Asp	Gly	Thr	Leu	Gly
		530				535					540				
Gly	Gln	Ala	Gln	Val	Asp	Asn	Val	Glu	Gly	Lys	Trp	Lys	Asp	Leu	Thr
545					550					555					560
Glu	Asn	Val	Asn	Thr	Met	Ala	Arg	Asn	Leu	Thr	Thr	Gln	Val	Arg	Gly
				565					570						575
Ile	Ser	Thr	Val	Thr	Gln	Ala	Ile	Ala	Asn	Gly	Asp	Met	Ser	Gln	Lys
			580					585					590		
Ile	Glu	Val	Ala	Ala	Ala	Gly	Glu	Ile	Leu	Ile	Leu	Lys	Glu	Thr	Ile
		595					600					605			
Asn	Asn	Met	Val	Asp	Arg	Leu	Ser	Ile	Phe	Ser	Asn	Glu	Val	Gln	Arg
		610				615					620				
Val	Ala	Lys	Asp	Val	Gly	Val	Asp	Gly	Lys	Met	Gly	Gly	Gln	Ala	Asp
625					630					635					640
Val	Ala	Gly	Ile	Gly	Gly	Arg	Trp	Lys	Glu	Ile	Thr	Thr	Asp	Val	Asn
				645					650						655
Thr	Met	Ala	Asn	Leu	Thr	Thr	Gln	Val	Arg	Ala	Phe	Gly	Asp	Ile	
			660				665					670			
Thr	Asn	Ala	Ala	Thr	Asp	Gly	Asp	Phe	Thr	Lys	Leu	Ile	Thr	Val	Glu
		675					680					685			
Ala	Ser	Gly	Glu	Met	Asp	Glu	Leu	Lys	Arg	Lys	Ile	Asn	Gln	Met	Val
		690				695					700				
Tyr	Asn	Leu	Arg	Asp	Ser	Ile	Gln	Arg	Asn	Thr	Leu	Ala	Arg	Glu	Ala
705					710					715					720
Ala	Glu	Phe	Ala	Asn	Arg	Thr	Lys	Ser	Glu	Phe	Leu	Ala	Asn	Met	Ser
				725					730						735
His	Glu	Ile	Arg	Thr	Pro	Met	Asn	Gly	Ile	Ile	Gly	Met	Thr	Gln	Leu
			740					745					750		
Thr	Leu	Asp	Thr	Asp	Leu	Thr	Gln	Tyr	Gln	Arg	Glu	Met	Leu	Asn	Ile
		755					760					765			
Val	His	Asn	Leu	Ala	Asn	Ser	Leu	Leu	Thr	Ile	Ile	Asp	Asp	Ile	Leu
		770				775					780				
Asp	Leu	Ser	Lys	Ile	Glu	Ala	Asn	Arg	Met	Ile	Met	Glu	Glu	Ile	Pro
785					790					795					800
Tyr	Thr	Leu	Arg	Gly	Thr	Val	Phe	Asn	Ala	Leu	Lys	Thr	Leu	Ala	Val
				805					810						815
Lys	Ala	Asn	Glu	Lys	Phe	Leu	Asp	Leu	Thr	Tyr	Arg	Val	Asp	Ser	Ser
			820					825					830		
Val	Pro	Asp	His	Val	Val	Gly	Asp	Ser	Phe	Arg	Leu	Arg	Gln	Val	Ile
		835					840					845			
Leu	Asn	Leu	Val	Gly	Asn	Ala	Ile	Lys	Phe	Thr	Glu	His	Gly	Glu	Val
		850				855					860				
Ser	Leu	Thr	Ile	Gln	Lys	Ala	Glu	Gln	Asp	His	Cys	Ala	Pro	Asn	Glu
865					870					875					880
Tyr	Ala	Val	Glu	Phe	Cys	Val	Ser	Asp	Thr	Gly	Ile	Gly	Ile	Gln	Ala
				885					890						895
Asp	Lys	Leu	Asn	Leu	Ile	Phe	Asp	Thr	Phe	Gln	Gln	Ala	Asp	Gly	Ser
			900					905						910	

Met	Thr	Arg	Lys	Phe	Gly	Gly	Thr	Gly	Leu	Gly	Leu	Ser	Ile	Ser	Lys
		915						920				925			
Arg	Leu	Val	Asn	Leu	Met	Arg	Gly	Asp	Val	Trp	Val	Lys	Ser	Gln	Tyr
		930					935					940			
Gly	Lys	Gly	Ser	Ser	Phe	Tyr	Phe	Thr	Cys	Thr	Val	Arg	Leu	Ala	Thr
		945				950					955				960
Ser	Asp	Ile	Ser	Phe	Ile	Gln	Lys	Gln	Leu	Lys	Pro	Tyr	Gln	Gly	His
				965						970					975
Asn	Val	Leu	Phe	Ile	Asp	Lys	Gly	Gln	Thr	Gly	His	Gly	Lys	Glu	Ile
			980						985					990	
Ile	Thr	Met	Leu	Thr	Gln	Leu	Gly	Leu	Val	Pro	Val	Val	Val	Asp	Ser
		995					1000					1005			
Glu	Gln	His	Thr	Ile	Leu	Leu	Gly	Asn	Gly	Arg	Thr	Lys	Glu	Lys	Ile
	1010					1015					1020				
Ala	Ser	Thr	Tyr	Asp	Val	Ile	Val	Val	Asp	Ser	Ile	Glu	Ser	Ala	Arg
	1025				1030					1035					1040
Lys	Leu	Arg	Ser	Ile	Asp	Glu	Phe	Lys	Tyr	Ile	Pro	Ile	Val	Leu	Leu
			1045						1050				1055		
Ala	Pro	Val	Ile	His	Val	Ser	Leu	Lys	Ser	Ala	Leu	Asp	Leu	Gly	Ile
		1060						1065					1070		
Thr	Ser	Tyr	Met	Thr	Thr	Pro	Cys	Leu	Thr	Ile	Asp	Leu	Gly	Asn	Gly
	1075					1080					1085				
Met	Ile	Pro	Ala	Leu	Glu	Asn	Arg	Ala	Ala	Pro	Ser	Leu	Ala	Asp	Asn
	1090					1095					1100				
Thr	Lys	Ser	Phe	Asp	Ile	Leu	Leu	Ala	Glu	Asp	Asn	Ile	Val	Asn	Gln
	1105				1110					1115					1120
Arg	Leu	Ala	Val	Lys	Ile	Leu	Glu	Lys	Tyr	His	His	Val	Val	Thr	Val
			1125						1130				1135		
Val	Gly	Asn	Gly	Gln	Glu	Ala	Leu	Asp	Ala	Ile	Lys	Glu	Lys	Arg	Tyr
		1140					1145					1150			
Asp	Val	Ile	Leu	Met	Asp	Val	Gln	Met	Pro	Ile	Met	Gly	Gly	Phe	Glu
	1155					1160					1165				
Ala	Thr	Ala	Lys	Ile	Arg	Glu	Tyr	Glu	Arg	Ser	Leu	Gly	Thr	Gln	Arg
	1170				1175					1180					
Thr	Pro	Ile	Ile	Ala	Leu	Thr	Ala	His	Ala	Met	Leu	Gly	Asp	Arg	Glu
	1185			1190					1195						1200
Lys	Cys	Ile	Gln	Ala	Gln	Met	Asp	Glu	Tyr	Leu	Ser	Lys	Pro	Leu	Lys
			1205						1210					1215	
Gln	Asn	His	Leu	Ile	Gln	Thr	Ile	Leu	Lys	Cys	Ala	Thr	Leu	Gly	Gly
		1220						1225				1230			
Ala	Leu	Leu	Glu	Lys	Gly	Arg	Glu	Val	Arg	Gln	Ser	Ala	Asn	Glu	Glu
	1235					1240					1245				
Ser	Pro	Asn	Ser	Gln	Asn	Gly	Pro	Arg	Gly	Thr	Gln	His	Pro	Ala	Ser
	1250				1255					1260					
Ser	Pro	Thr	Pro	Ala	His	Met	Arg	Pro	Ala	Ile	Glu	Pro	Arg	Ala	Tyr
	1265			1270					1275						1280
Thr	Thr	Thr	Gly	Pro	Ile	Asn	His	Gly	Ser	Ala	Glu	Ser	Pro	Ser	Leu
			1285					1290					1295		
Val	Thr	Ala	Asp	Ala	Glu	Asp	Pro	Leu	Ala	Arg	Leu	Leu	Met	Arg	Ala
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His	Ser	Ser													
		1315													

<210> 14

<211> 3948

<212> DNA

<213> Botryotinia fuckeliana

<220>

<221> CDS

<222> (1)..(3948)

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gca tta tcg agc atc gat ctt cca ctg acg aat gtt tac ggc aac aag	96
Ala Leu Ser Ser Ile Asp Leu Pro Leu Thr Asn Val Tyr Gly Asn Lys	
20 25 30	
ggg att agg tta cca ggt gca gat acg gca gag aag ctt gcc ctc gaa	144
Gly Ile Arg Leu Pro Gly Ala Asp Thr Ala Glu Lys Leu Ala Leu Glu	
35 40 45	
cga gaa ctt gcg gcc ttg gta tcc aga gtc caa aga tta gaa gca agg	192
Arg Glu Leu Ala Ala Leu Val Ser Arg Val Gln Arg Leu Glu Ala Arg	
50 55 60	
gcg atc aca gtc aat aat caa acc ctg ccc gat acg ccg aat gaa tta	240
Ala Ile Thr Val Asn Asn Gln Thr Leu Pro Asp Thr Pro Asn Glu Leu	
65 70 75 80	
gga gcg cca tct gct ttc gca gat gta ctc act ggt gcc cca tcc cga	288
Gly Ala Pro Ser Ala Phe Ala Asp Val Leu Thr Gly Ala Pro Ser Arg	
85 90 95	
gcc tca aag agt act aca tcc cga caa cag ctc gta aat tcg ttg ctt	336
Ala Ser Lys Ser Thr Thr Ser Arg Gln Gln Leu Val Asn Ser Leu Leu	
100 105 110	
gcc gcc aga gaa gcg ccc acc ggc ggt gaa aga cct cct aaa ttt acg	384
Ala Ala Arg Glu Ala Pro Thr Gly Gly Glu Arg Pro Pro Lys Phe Thr	
115 120 125	
aaa tta agt gac gag gaa ctc gaa gca ctc cgc gaa cat gtc gac cat	432
Lys Leu Ser Asp Glu Glu Leu Glu Ala Leu Arg Glu His Val Asp His	
130 135 140	
caa tcg aaa caa ctc gat agt caa aaa tct gag ctg gcc ggt gta cat	480
Gln Ser Lys Gln Leu Asp Ser Gln Lys Ser Glu Leu Ala Gly Val His	
145 150 155 160	
gct caa ctg ttt gag cag aag cag aga caa gaa caa gca ctc aac gtt	528
Ala Gln Leu Phe Glu Gln Lys Gln Arg Gln Glu Gln Ala Leu Asn Val	
165 170 175	
ctt gaa gtc gaa cgc gta gca gct ctc gaa aga gaa ctg aag aag cat	576
Leu Glu Val Glu Arg Val Ala Ala Leu Glu Arg Glu Leu Lys Lys His	
180 185 190	
caa caa gcc aac gag gct ttc caa aaa gct cta cgg gaa ata gga gag	624
Gln Gln Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Glu	
195 200 205	
att gtc aca gct gta gct agg ggt gat ctc agt aag aag gta caa atc	672
Ile Val Thr Ala Val Ala Arg Gly Asp Leu Ser Lys Lys Val Gln Ile	
210 215 220	

cac	tcc	gtg	gag	atg	gac	cct	gag	att	aca	act	ttc	aag	cgt	gtt	att	720
His	Ser	Val	Glu	Met	Asp	Pro	Glu	Ile	Thr	Thr	Phe	Lys	Arg	Val	Ile	
225					230					235					240	
aat	act	atg	atg	gat	caa	ctt	cag	ata	ttc	tct	agt	gag	gtt	tct	cgt	768
Asn	Thr	Met	Met	Asp	Gln	Leu	Gln	Ile	Phe	Ser	Ser	Glu	Val	Ser	Arg	
				245					250					255		
gta	gct	aga	gag	gtc	ggc	aca	gaa	ggg	att	ctc	ggg	gga	caa	gcc	aag	816
Val	Ala	Arg	Glu	Val	Gly	Thr	Glu	Gly	Ile	Leu	Gly	Gly	Gln	Ala	Lys	
			260					265					270			
att	tct	ggg	gtt	gat	ggg	aca	tgg	aag	gag	ttg	act	gac	aat	gtc	aac	864
Ile	Ser	Gly	Val	Asp	Gly	Thr	Trp	Lys	Glu	Leu	Thr	Asp	Asn	Val	Asn	
		275					280					285				
gtt	atg	gca	caa	aat	ctc	acc	gat	caa	gtc	cga	gaa	att	gct	tcc	gtc	912
Val	Met	Ala	Gln	Asn	Leu	Thr	Asp	Gln	Val	Arg	Glu	Ile	Ala	Ser	Val	
	290					295					300					
act	act	gct	gta	gct	cat	gga	gat	ctc	aca	caa	aag	att	gag	aga	cca	960
Thr	Thr	Ala	Val	Ala	His	Gly	Asp	Leu	Thr	Gln	Lys	Ile	Glu	Arg	Pro	
305					310					315					320	
gcc	cag	ggg	gag	ata	ctc	caa	ctg	caa	caa	act	atc	aat	acc	atg	gtg	1008
Ala	Gln	Gly	Glu	Ile	Leu	Gln	Leu	Gln	Gln	Thr	Ile	Asn	Thr	Met	Val	
				325				330						335		
gat	caa	ttg	aga	acg	ttc	gcc	gcc	gag	gtc	acc	cgc	gta	gca	aga	gat	1056
Asp	Gln	Leu	Arg	Thr	Phe	Ala	Ala	Glu	Val	Thr	Arg	Val	Ala	Arg	Asp	
			340					345					350			
gta	gga	act	gaa	ggg	att	ctt	ggg	ggg	caa	gca	gaa	agc	gaa	ggc	gtc	1104
Val	Gly	Thr	Glu	Gly	Ile	Leu	Gly	Gly	Gln	Ala	Glu	Ser	Glu	Gly	Val	
		355					360					365				
cag	ggc	atg	tgg	aac	aca	ttg	ata	gtg	aac	gtc	aac	gct	atg	gcc	aat	1152
Gln	Gly	Met	Trp	Asn	Thr	Leu	Ile	Val	Asn	Val	Asn	Ala	Met	Ala	Asn	
	370					375					380					
aac	ctc	acc	aca	caa	gtg	cgc	gat	ata	gcc	att	gtc	aca	aca	gct	gtc	1200
Asn	Leu	Thr	Thr	Gln	Val	Arg	Asp	Ile	Ala	Ile	Val	Thr	Thr	Ala	Val	
385					390					395					400	
gca	aag	gga	gac	ctg	act	caa	aag	gtc	caa	gca	gaa	tgt	aag	ggg	gaa	1248
Ala	Lys	Gly	Asp	Leu	Thr	Gln	Lys	Val	Gln	Ala	Glu	Cys	Lys	Gly	Glu	
			405						410					415		
atc	aag	cag	ttg	aag	gag	act	ata	aat	tcc	atg	gtg	gac	caa	tta	caa	1296
Ile	Lys	Gln	Leu	Lys	Glu	Thr	Ile	Asn	Ser	Met	Val	Asp	Gln	Leu	Gln	
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Gln	Phe	Ala	Arg	Glu	Val	Thr	Lys	Ile	Ala	Arg	Glu	Val	Gly	Thr	Glu	
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Gly	Arg	Leu	Gly	Gly	Gln	Ala	Thr	Val	His	Asp	Val	Glu	Gly	Thr	Trp	
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Arg Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr	
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caa gta cga gag att gca aag gtt acc acc gct gtc gcc aga gga gat	1488
Gln Val Arg Glu Ile Ala Lys Val Thr Thr Ala Val Ala Arg Gly Asp	
485 490 495	
ttg acc aag aag att gaa gtc gag gtt cag gga gaa atc gct tcg ctg	1536
Leu Thr Lys Lys Ile Glu Val Glu Val Gln Gly Glu Ile Ala Ser Leu	
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Lys Asp Thr Ile Asn Thr Met Val Asp Arg Leu Ser Thr Phe Ala Phe	
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Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr Leu Gly	
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Gly Gln Ala Gln Val Asp Asn Val Glu Gly Lys Trp Lys Asp Leu Thr	
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Glu Asn Val Asn Thr Met Ala Arg Asn Leu Thr Thr Gln Val Arg Gly	
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Ile Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Gln Lys	
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Ile Glu Val Ala Ala Ala Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile	
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Asn Asn Met Val Asp Arg Leu Ser Ile Phe Ser Asn Glu Val Gln Arg	
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Val Ala Lys Asp Val Gly Val Asp Gly Lys Met Gly Gly Gln Ala Asp	
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675 680 685	
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Ala Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln Met Val	
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Ala Glu Phe Ala Asn Arg Thr Lys Ser Glu Phe Leu Ala Asn Met Ser	
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cac gag att cga aca cct atg aac ggt atc att ggt atg act cag ttg	2256
His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu	
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Thr Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile	
755 760 765	
gtt cac aac ttg gcc aac agt tta ttg acc atc att gat gat att ctc	2352
Val His Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu	
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785 790 795 800	
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Tyr Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val	
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Lys Ala Asn Glu Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp Ser Ser	
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Ser Leu Thr Ile Gln Lys Ala Glu Gln Asp His Cys Ala Pro Asn Glu	
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Tyr Ala Val Glu Phe Cys Val Ser Asp Thr Gly Ile Gly Ile Gln Ala	
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atg acg agg aaa ttc gga ggt act ggt cta ggt cta tca att tcg aag	2784
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915 920 925	
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Gly Lys Gly Ser Ser Phe Tyr Phe Thr Cys Thr Val Arg Leu Ala Thr	
945 950 955 960	
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Ser Asp Ile Ser Phe Ile Gln Lys Gln Leu Lys Pro Tyr Gln Gly His	
965 970 975	
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Asn Val Leu Phe Ile Asp Lys Gly Gln Thr Gly His Gly Lys Glu Ile	
980 985 990	
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Ile Thr Met Leu Thr Gln Leu Gly Leu Val Pro Val Val Val Asp Ser	
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Thr Lys Ser Phe Asp Ile Leu Leu Ala Glu Asp Asn Ile Val Asn Gln	
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Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr Val	
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Val Gly Asn Gly Gln Glu Ala Leu Asp Ala Ile Lys Glu Lys Arg Tyr	
1140 1145 1150	
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Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly Gly Phe Glu	
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Ala Thr Ala Lys Ile Arg Glu Tyr Glu Arg Ser Leu Gly Thr Gln Arg	
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1185 1190 1195 1200	
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Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Lys	
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Gln Asn His Leu Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly	
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Ser Pro Thr Pro Ala His Met Arg Pro Ala Ile Glu Pro Arg Ala Tyr	
1265 1270 1275 1280	
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His Ser Ser	
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 oligonucleotide primer for PCR

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Thr 65	Arg	Ala	Asn	Ala	Ala 70	Pro	Ala	Thr	Ile	Phe 75	Pro	Asp	Thr	Pro	Asn 80	
Glu	Thr	Ala	His	Ser 85	Leu	Phe	Gly	Asp	Asp 90	Ser	Ser	Ser	Pro	Thr 95	Ser	
Ser	Ser	Ser	Gly 100	Arg	Glu	Pro	Lys	Arg 105	Leu	Lys	Ser	Ala	Ser	Ser	Thr	
Thr	Arg	Asn 115	Gly	Phe	Thr	Thr	Asp 120	Gly	Arg	Pro	Ser	Lys 125	Leu	Asn	Ala	
Ile 130	Thr	Asp	Glu	Glu	Leu	Glu 135	Gly	Leu	Arg	Glu	His 140	Val	Asp	Gly	Gln	
Ser 145	Arg	Leu	Leu	Asp	Ser 150	Gln	Arg	Ala	Glu	Leu 155	Asp	Gly	Val	Asn	Ala 160	
Gln	Leu	Leu	Glu	Gln 165	Lys	Gln	Leu	Gln	Glu	Arg 170	Ala	Leu	Ala	Ile 175	Ile	
Glu 180	Gln	Glu	Arg	Val 185	Ala	Thr	Leu	Glu	Arg	Glu 190	Leu	Trp	Lys	His	Gln	
Lys	Ala	Asn 195	Glu	Ala	Phe	Gln 200	Lys	Ala	Leu	Arg	Glu 205	Ile	Gly	Ser	Ile	
Val 210	Thr	Ala	Ala	Ala	Arg	Gly 215	Asp	Leu	Ser	Lys	Arg 220	Val	Lys	Ile	Asn	
Pro 225	Ile	Glu	Met	Asp	Pro 230	Glu	Ile	Thr	Thr	Phe 235	Lys	Arg	Thr	Met	Asn 240	
Ala	Met	Met	Asp	Gln 245	Leu	Gly	Val	Phe	Ser 250	Ser	Glu	Val	Ser	Arg 255	Val	
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Thr 305	Ala	Val	Ala	His	Gly 310	Asp	Leu	Thr	Gln	Lys 315	Ile	Glu	Ser	Ala	Ala 320	
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Gln	Leu	Arg	Thr 340	Phe	Ala	Ser	Glu	Val 345	Thr	Arg	Val	Ala	Arg	Asp	Val	
Gly	Thr	Glu 355	Gly	Met	Leu	Gly	Gly 360	Gln	Ala	Asp	Val	Glu	Gly	Val	Lys	
Gly	Met	Trp 370	Asn	Glu	Leu	Thr	Val 375	Asn	Val	Asn	Ala 380	Met	Ala	Asn	Asn	
Leu 385	Thr	Thr	Gln	Val	Arg	Asp 390	Ile	Ile	Asn	Val 395	Thr	Thr	Ala	Val	Ala 400	
Lys	Gly	Asp	Leu	Thr 405	Gln	Lys	Val	Gln	Ala 410	Glu	Cys	Arg	Gly	Glu	Ile	
Phe	Glu	Leu	Lys 420	Asn	Thr	Ile	Asn	Ser 425	Met	Val	Asp	Gln	Leu	Gln	Gln	
Phe	Ala	Arg 435	Glu	Val	Thr	Lys	Ile 440	Ala	Arg	Glu	Val	Gly 445	Thr	Glu	Gly	
Arg	Leu	Gly 450	Gly	Gln	Ala	Thr 455	Val	His	Asp	Val	Gln 460	Gly	Thr	Trp	Arg	
Asp 465	Leu	Thr	Glu	Asn	Val	Asn 470	Gly	Met	Ala	Met 475	Asn	Leu	Thr	Thr	Gln 480	
Val	Arg	Glu	Ile	Ala 485	Asn	Val	Thr	Ser	Ala 490	Val	Ala	Ala	Gly	Asp	Leu 495	
Ser	Lys	Lys	Ile 500	Arg	Val	Glu	Val	Lys 505	Gly	Glu	Ile	Leu	Asp	Leu	Lys	
Asn	Thr	Ile 515	Asn	Thr	Met	Val	Asp 520	Arg	Leu	Gly	Thr	Phe 525	Ala	Phe	Glu	

Val	Ser	Lys	Val	Ala	Arg	Ala	Val	Gly	Thr	Asp	Gly	Thr	Leu	Gly	Gly
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Ala	Gly	Leu	Lys	Gly	Arg	Trp	Lys	Glu	Ile	Thr	Thr	Asp	Val	Asn	Thr
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Glu	Leu	Ala	Asn	Lys	Thr	Lys	Ser	Glu	Phe	Leu	Ala	Asn	Met	Ser	His
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Leu	Asp	Thr	Asp	Leu	Thr	Gln	Tyr	Gln	Arg	Glu	Met	Leu	Asn	Ile	Val
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Met	Ile	Glu	Phe	Val	Val	Ser	Asp	Thr	Gly	Ile	Gly	Ile			

Gln Asn His Thr Leu Thr Arg Val Arg Gly Lys Glu Cys Pro Tyr Asp
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 1090 1095 1100
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 Ile Ala Thr Asn Ser Gly Ala Pro Gly Lys Asn Ala Ser Phe Arg Ser
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 Ser Thr Tyr Val Gln Leu Pro Gly Pro Glu Ser Asp Glu Lys Lys Gln
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Leu Glu Arg Glu Leu Ala Ala Leu Val Ile Arg Val Gln Gln Leu Glu	
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Thr Arg Ala Asn Ala Ala Pro Ala Thr Ile Phe Pro Asp Thr Pro Asn	
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Glu Thr Ala His Ser Leu Phe Gly Asp Asp Ser Ser Ser Pro Thr Ser	
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Ser Ser Ser Gly Arg Glu Pro Lys Arg Leu Lys Ser Ala Ser Ser Thr	
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Lys Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Ser Ile	
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Val Thr Ala Ala Ala Arg Gly Asp Leu Ser Lys Arg Val Lys Ile Asn	
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gcc atg atg gat caa ctt ggc gtc ttc tct agt gaa gtc tcg cga gtg	768
Ala Met Met Asp Gln Leu Gly Val Phe Ser Ser Glu Val Ser Arg Val	
245 250 255	
gca aga gag gtc ggc acc gag ggc ata tta ggt gga cag gcc cag atc	816
Ala Arg Glu Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Gln Ile	
260 265 270	
gag gga gtg gac ggc acg tgg aaa gaa ctg acg gac aat gtc aac gtc	864
Glu Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn Val Asn Val	
275 280 285	

atg gcg cag aac ctg acc gac caa gtc cgc gaa atc gcc tca gtc act	912
Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala Ser Val Thr	
290 295 300	
aca gct gtg gcc cac gga gat ttg acc caa aag att gag agt gcg gcc	960
Thr Ala Val Ala His Gly Asp Leu Thr Gln Lys Ile Glu Ser Ala Ala	
305 310 315 320	
aag gga gaa atc cta cag ctt caa caa act ata, aat acc atg gtg gac	1008
Lys Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr Met Val Asp	
325 330 335	
caa cta cgc aca ttt gct tca gag gtt acc cgt gtc gcc cgt gac gtc	1056
Gln Leu Arg Thr Phe Ala Ser Glu Val Thr Arg Val Ala Arg Asp Val	
340 345 350	
gga acc gag gga atg ctc ggc ggg cag gct gac gtt gaa ggg gtc aag	1104
Gly Thr Glu Gly Met Leu Gly Gly Gln Ala Asp Val Glu Gly Val Lys	
355 360 365	
ggc atg tgg aat gag ctg acg gtc aac gtc aac gcc atg gcc aac aat	1152
Gly Met Trp Asn Glu Leu Thr Val Asn Val Asn Ala Met Ala Asn Asn	
370 375 380	
tta aca acc caa gtg cgc gac atc atc aac gtt acc aca gcc gtc gca	1200
Leu Thr Thr Gln Val Arg Asp Ile Ile Asn Val Thr Thr Ala Val Ala	
385 390 395 400	
aag gga gat ctt aca caa aag gtg cag gcg gaa tgt cgc ggc gag att	1248
Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Arg Gly Glu Ile	
405 410 415	
ttt gag ctc aag aac acg atc aat tcc atg gtg gac cag ctg cag caa	1296
Phe Glu Leu Lys Asn Thr Ile Asn Ser Met Val Asp Gln Leu Gln Gln	
420 425 430	
ttt gct cgc gag gtt acc aag atc gcc aga gag gtt ggt acc gaa gga	1344
Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu Gly	
435 440 445	
cgg ctg ggc ggc caa gca act gtt cac gat gta cag gga act tgg cga	1392
Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Gln Gly Thr Trp Arg	
450 455 460	
gat ctc aca gaa aac gtg aac gga atg gct atg aat ctc acc aca caa	1440
Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr Gln	
465 470 475 480	
gta cga gag ata gcc aat gtt acc agt gcc gtc gct gca ggc gac cta	1488
Val Arg Glu Ile Ala Asn Val Thr Ser Ala Val Ala Ala Gly Asp Leu	
485 490 495	
tcc aag aag atc agg gta gag gtc aag ggc gag att ctg gac ctc aaa	1536
Ser Lys Lys Ile Arg Val Glu Val Lys Gly Glu Ile Leu Asp Leu Lys	
500 505 510	
aat acc atc aac acc atg gtt gac cgc ctc gga act ttc gcc ttc gaa	1584
Asn Thr Ile Asn Thr Met Val Asp Arg Leu Gly Thr Phe Ala Phe Glu	
515 520 525	

gtc agc aaa gta gcc cga gcc gtc ggc aca gat ggc act ctt ggt ggt	1632
Val Ser Lys Val Ala Arg Ala Val Gly Thr Asp Gly Thr Leu Gly Gly	
530 535 540	
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Gln Ala Gln Val Glu Asn Val Glu Gly Lys Trp Lys Asp Leu Thr Glu	
545 550 555 560	
aac gtc aac acc atg gcg tca aac ctc act tct cag gtc agg gga ata	1728
Asn Val Asn Thr Met Ala Ser Asn Leu Thr Ser Gln Val Arg Gly Ile	
565 570 575	
tca acc gtg aca caa gcc atc gcg aac ggt gac atg agc cga aag atc	1776
Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Arg Lys Ile	
580 585 590	
gac gtg gaa gcc aag ggc gag ata cta atc ctc aag gaa act atc aac	1824
Asp Val Glu Ala Lys Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile Asn	
595 600 605	
aac atg gtt gat cgt ctg tcg ata ttc tgc aat gaa gta caa cga gtc	1872
Asn Met Val Asp Arg Leu Ser Ile Phe Cys Asn Glu Val Gln Arg Val	
610 615 620	
gca aaa gat gta ggc gtt gat ggc att atg ggg gga caa gcc gac gtt	1920
Ala Lys Asp Val Gly Val Asp Gly Ile Met Gly Gly Gln Ala Asp Val	
625 630 635 640	
gca ggt ctc aag ggg cga tgg aag gag att acc acc gat gtc aac acc	1968
Ala Gly Leu Lys Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn Thr	
645 650 655	
atg gcc aac aat ctt acg gcg caa gta cgc gct ttc gga gat ata acc	2016
Met Ala Asn Asn Leu Thr Ala Gln Val Arg Ala Phe Gly Asp Ile Thr	
660 665 670	
aat gcc gct acc gac gga gac ttc acc aag ctg gtc gag gtt gag gcg	2064
Asn Ala Ala Thr Asp Gly Asp Phe Thr Lys Leu Val Glu Val Glu Ala	
675 680 685	
tcg ggc gaa atg gac gaa ctg aag cgc aag atc aat caa atg gtc tac	2112
Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln Met Val Tyr	
690 695 700	
aat ctc cga gac agt atc caa aga aac acg caa gca aga gaa gcc gca	2160
Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Gln Ala Arg Glu Ala Ala	
705 710 715 720	
gaa ttg gcc aac aag acg aag tcg gag ttc ctc gct aac atg tcc cac	2208
Glu Leu Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn Met Ser His	
725 730 735	
gaa atc cgc aca ccc atg aac ggt atc atc ggc atg aca caa ctt act	2256
Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu Thr	
740 745 750	
ctt gat aca gat ttg acg caa tac caa cgc gaa atg ctc aac att gtc	2304
Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile Val	
755 760 765	

aac aat ctc gcc atg agt ctg ctc acc att atc gac gac atc ctc gat	2352
Asn Asn Leu Ala Met Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu Asp	
770 775 780	
ctg tca aag att gag gct aag cgg atg gtt atc gag gag att cca tac	2400
Leu Ser Lys Ile Glu Ala Lys Arg Met Val Ile Glu Glu Ile Pro Tyr	
785 790 795 800	
acg tta cga gga acg gtc ttc aac gca ctg aag act ttg gcg gtc aag	2448
Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val Lys	
805 810 815	
gcg aac gac aag ttt ttg gat ctc acg tac cgt gtg gac agc tca gtt	2496
Ala Asn Asp Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp Ser Ser Val	
820 825 830	
cct gac cac gtc atc ggt gac tcg ttc cgt ctg cgc cag att atc ctg	2544
Pro Asp His Val Ile Gly Asp Ser Phe Arg Leu Arg Gln Ile Ile Leu	
835 840 845	
aac ctg gtt ggc aat gcc atc aaa ttc acc gag cat gga gag gtc agc	2592
Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val Ser	
850 855 860	
ctt act atc cag aag ggc aac gac gtg acg tgc ctg cca aac gag tac	2640
Leu Thr Ile Gln Lys Gly Asn Asp Val Thr Cys Leu Pro Asn Glu Tyr	
865 870 875 880	
atg atc gaa ttt gtc gtg tcg gac acg ggc ata gga att cca acg gac	2688
Met Ile Glu Phe Val Val Ser Asp Thr Gly Ile Gly Ile Pro Thr Asp	
885 890 895	
aaa ctg ggt ctc atc ttc gac aca ttc cag cag gct gat gga tcc atg	2736
Lys Leu Gly Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser Met	
900 905 910	
aca cgc aag ttt ggc gga acc ggg ctt ggt ctg tct att tcc aag agg	2784
Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Arg	
915 920 925	
ctc gtc aac ctc atg ggc ggt gac gtg tgg gtc aag tca caa tac ggc	2832
Leu Val Asn Leu Met Gly Gly Asp Val Trp Val Lys Ser Gln Tyr Gly	
930 935 940	
aag ggc agc tcg ttc tac ttc act tgt cgt gtc cgc ctc gcc gac gtg	2880
Lys Gly Ser Ser Phe Tyr Phe Thr Cys Arg Val Arg Leu Ala Asp Val	
945 950 955 960	
gat atc tca ctc atc agg aag cag ctg aag cct tac aag gga cac cag	2928
Asp Ile Ser Leu Ile Arg Lys Gln Leu Lys Pro Tyr Lys Gly His Gln	
965 970 975	
gtc ctg ttc atc gat aag ggc aag act gga cac ggg ccc gag gtg ggg	2976
Val Leu Phe Ile Asp Lys Gly Lys Thr Gly His Gly Pro Glu Val Gly	
980 985 990	
cag atg ctc ggc cag ctg ggt ttg gtg ccc atc gtg ctg gaa tcc gag	3024
Gln Met Leu Gly Gln Leu Gly Leu Val Pro Ile Val Leu Glu Ser Glu	
995 1000 1005	

caa aat cac acc ctg acg cgg gtg cgc ggc aag gaa tgt ccc tac gac	3072
Gln Asn His Thr Leu Thr Arg Val Arg Gly Lys Glu Cys Pro Tyr Asp	
1010 1015 1020	
gtg ata gtt gtc gac tca atc gac aca gcc cgg cgc ctg aga gga att	3120
Val Ile Val Val Asp Ser Ile Asp Thr Ala Arg Arg Leu Arg Gly Ile	
1025 1030 1035 1040	
gac gac ttc aag tat ctg ccc atc gtt ctc ctg gcg cca act gtc cac	3168
Asp Asp Phe Lys Tyr Leu Pro Ile Val Leu Leu Ala Pro Thr Val His	
1045 1050 1055	
gtc agc ctg aaa tcc tgc ttg gac ttg ggt att acc tcg tat atg acg	3216
Val Ser Leu Lys Ser Cys Leu Asp Leu Gly Ile Thr Ser Tyr Met Thr	
1060 1065 1070	
atg ccc tgc aag ctc atc gac ctc ggc aat ggt atg gtt ccc gct ctt	3264
Met Pro Cys Lys Leu Ile Asp Leu Gly Asn Gly Met Val Pro Ala Leu	
1075 1080 1085	
gag aac cgt gcc aca cca tca cta tca gac aac act aag tcg ttc gaa	3312
Glu Asn Arg Ala Thr Pro Ser Leu Ser Asp Asn Thr Lys Ser Phe Glu	
1090 1095 1100	
att ctg ctg gcc gag gac aac acc gtc aac cag cgc ctg gcc gtt aag	3360
Ile Leu Leu Ala Glu Asp Asn Thr Val Asn Gln Arg Leu Ala Val Lys	
1105 1110 1115 1120	
att ctt gaa aag tac aac cac gtt gtg acg gta gtc agc aac ggt gct	3408
Ile Leu Glu Lys Tyr Asn His Val Val Thr Val Val Ser Asn Gly Ala	
1125 1130 1135	
gaa gct ctt gaa gct gtc aag gat aac aaa tac gat gtg atc ctg atg	3456
Glu Ala Leu Glu Ala Val Lys Asp Asn Lys Tyr Asp Val Ile Leu Met	
1140 1145 1150	
gat gtt caa atg cct gtc atg ggt gga ttt gag gcg acg gca aag att	3504
Asp Val Gln Met Pro Val Met Gly Phe Glu Ala Thr Ala Lys Ile	
1155 1160 1165	
cgt gaa tac gag cgc agc ctg ggc aca cag agg aca cca atc atc gcg	3552
Arg Glu Tyr Glu Arg Ser Leu Gly Thr Gln Arg Thr Pro Ile Ile Ala	
1170 1175 1180	
ctt acc gct cac gca atg atg ggc gac cgt gag aag tgt atc gag gcc	3600
Leu Thr Ala His Ala Met Met Gly Asp Arg Glu Lys Cys Ile Glu Ala	
1185 1190 1195 1200	
cag atg gac gag tac ctg tcg aag cct ctg cag cag aac cac ttg ata	3648
Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Gln Gln Asn His Leu Ile	
1205 1210 1215	
caa aca att ctc aag tgt gca acg ctg ggt ggc gcc ttg ttg gaa caa	3696
Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly Ala Leu Leu Glu Gln	
1220 1225 1230	
aat cgt gag cgc gag ctt gaa cta gca agg cat gcc gaa cac aaa gga	3744
Asn Arg Glu Arg Glu Leu Glu Leu Ala Arg His Ala Glu His Lys Gly	
1235 1240 1245	

gga ctg tct acg gac ccg gcg agg gca tcg tcg gta atg cgt ccg cca	3792
Gly Leu Ser Thr Asp Pro Ala Arg Ala Ser Ser Val Met Arg Pro Pro	
1250 1255 1260	

cta cac cac cga ccg gtg act aca gcc gag tcg ctt tct ggt ggc gcc	3840
Leu His His Arg Pro Val Thr Thr Ala Glu Ser Leu Ser Gly Gly Ala	
1265 1270 1275 1280	

gaa agc ccc tcg ttg atg gca aat gac ggc gaa gat cca ata caa agg	3888
Glu Ser Pro Ser Leu Met Ala Asn Asp Gly Glu Asp Pro Ile Gln Arg	
1285 1290 1295	

gca cgt agc agt ctc tct gaa cca gga tgc cta taa	3924
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

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<210> 19
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<220>
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<400> 19	
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<210> 20
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<220>
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<220>
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<400> 21
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 <211> 25
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<220>
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<400> 22
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<400> 24
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 <400> 26
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 <210> 27
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 <400> 27
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 <400> 28
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 <210> 29
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 <212> DNA
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 <220>
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 <400> 29
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 <210> 30
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 <212> DNA
 <213> Artificial Sequence

 <220>
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<400> 30
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<210> 31
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 <213> Artificial Sequence

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<400> 31
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<210> 32
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<400> 32
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<210> 33
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<400> 33
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<210> 34
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<210> 35
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<400> 35
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<400> 36
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<210> 37
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<400> 37
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<210> 40
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 <212> DNA
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26

<210> 41
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 20 25 30
 Ser Gln Val Gln Leu Pro Gly Pro Asp Thr Pro Ala Lys Arg Lys Leu
 35 40 45
 Glu Leu Glu Leu Gln Asn Leu Ala Leu Arg Val Gly Lys Leu Glu Ser
 50 55 60
 Gln Ala Ser Ala Thr Ser Pro Phe Pro Glu Thr Pro Asn Glu Val Ile
 65 70 75 80
 Asp Thr Leu Phe Gly Glu Glu Ala Gln Ala Val Ala Val Arg Pro Lys
 85 90 95
 Pro Lys Val Phe His Ala Gln Gly Ser Leu His Ser Pro His Leu Pro
 100 105 110
 Ser Tyr Gln Leu Thr Glu Glu Ala Leu Glu Gly Leu Arg Glu His Val
 115 120 125
 Asp Asp Gln Ser Lys Leu Leu Asp Ser Gln Arg Gln Glu Leu Ala Gly
 130 135 140
 Val Asn Ala Gln Leu Leu Glu Gln Lys Gln Leu Glu Arg Ala Leu
 145 150 155 160
 Glu Ile Leu Glu Gln Glu Arg Ile Ala Thr Leu Glu Arg Glu Leu Trp
 165 170 175
 Lys His Gln Lys Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile
 180 185 190
 Gly Glu Ile Val Thr Ala Val Ala Arg Gly Asp Leu Thr Met Lys Val
 195 200 205
 Arg Met Asn Thr Val Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg
 210 215 220
 Thr Ile Asn Ala Met Met Asp Gln Leu Gln Ile Phe Ala Ser Glu Val
 225 230 235 240
 Ser Arg Val Ala Arg Glu Val Gly Thr Glu Gly Leu Leu Gly Gly Gln
 245 250 255
 Ala Arg Ile Gly Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn
 260 265 270
 Val Asn Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala
 275 280 285
 Ser Val Thr Thr Ala Val Ala His Gly Asp Leu Thr Lys Lys Ile Glu
 290 295 300
 Arg Pro Ala Arg Gly Glu Ile Leu Gln Leu Gln Thr Ile Asn Thr
 305 310 315 320
 Met Val Asp Gln Leu Arg Thr Phe Ala Ser Glu Val Thr Arg Val Ala
 325 330 335

Arg	Asp	Val	Gly	Thr	Glu	Gly	Met	Leu	Gly	Gly	Gln	Ala	Asp	Val	Gly
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	370					375					380				
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Gly	Glu	Ile	Phe	Glu	Leu	Lys	Ser	Thr	Ile	Asn	Ser	Met	Val	Asp	Gln
				405					410					415	
Leu	Gln	Gln	Phe	Ala	Arg	Glu	Val	Thr	Lys	Ile	Ala	Arg	Glu	Val	Gly
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Thr	Glu	Gly	Arg	Leu	Gly	Gly	Gln	Ala	Thr	Val	His	Asp	Val	Glu	Gly
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Gly	Asp	Leu	Thr	Lys	Lys	Ile	Gly	Val	Glu	Val	Lys	Gly	Glu	Ile	Ala
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Glu	Leu	Lys	Asn	Thr	Ile	Asn	Gln	Met	Val	Asp	Arg	Leu	Gly	Thr	Phe
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Ala	Val	Glu	Val	Ser	Lys	Val	Ala	Arg	Glu	Val	Gly	Thr	Asp	Gly	Thr
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Leu	Gly	Gly	Gln	Ala	Gln	Val	Ala	Asn	Val	Glu	Gly	Lys	Trp	Lys	Asp
	530					535					540				
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Arg	Ser	Ile	Ser	Thr	Val	Thr	Gln	Ala	Ile	Ala	Asn	Gly	Asp	Met	Ser
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Val	Asn	Thr	Met	Ala	Ser	Asn	Leu	Thr	Thr	Gln	Val	Arg	Ala	Phe	Ser
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Asp	Ile	Thr	Asn	Leu	Ala	Thr	Asp	Gly	Asp	Phe	Thr	Lys	Leu	Val	Asp
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Val	Glu	Ala	Ser	Gly	Glu	Met	Asp	Glu	Leu	Lys	Arg	Lys	Ile	Asn	Gln
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Met	Ile														

Ser	Ser	Val	Pro	Asp	Tyr	Val	Ile	Gly	Asp	Ser	Phe	Arg	Leu	Arg	Gln
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Ile	Ile	Leu	Asn	Leu	Val	Gly	Asn	Ala	Ile	Lys	Phe	Thr	Glu	His	Gly
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	850					855					860				
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865					870					875					880
Ile	Ala	Gln	Asp	Lys	Leu	Asp	Leu	Ile	Phe	Asp	Thr	Phe	Gln	Gln	Ala
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Asp	Gly	Ser	Met	Thr	Arg	Lys	Phe	Gly	Gly	Thr	Gly	Leu	Gly	Leu	Ser
			900					905					910		
Ile	Ser	Lys	Arg	Leu	Val	Asn	Leu	Met	Gly	Gly	Asp	Leu	Trp	Val	Asn
		915					920					925			
Ser	Glu	His	Gly	Lys	Gly	Ser	Glu	Phe	His	Phe	Thr	Cys	Leu	Val	Lys
	930					935					940				
Leu	Ala	Pro	Asp	Asp	Ala	Ala	Leu	Ile	Glu	Gln	Gln	Ile	Arg	Pro	Tyr
945					950					955					960
Arg	Gly	His	Gln	Val	Leu	Phe	Val	Asp	Lys	Ala	Gln	Ser	Gln	Asn	Ala
				965					970					975	
Thr	Ser	Ile	Lys	Pro	Met	Leu	Glu	Lys	Ile	Gly	Leu	Lys	Pro	Val	Val
			980					985					990		
Val	Asp	Ser	Glu	Lys	Ser	Pro	Ala	Leu	Thr	Arg	Leu	Gln	Ser	Gly	Gly
		995				1000						1005			
Ser	Leu	Pro	Tyr	Asp	Ala	Ile	Leu	Val	Asp	Ser	Ile	Asp	Thr	Ala	Arg
	1010					1015					1020				
Arg	Leu	Arg	Ala	Val	Asp	Asp	Phe	Lys	Tyr	Leu	Pro	Ile	Val	Leu	Leu
1025				1030						1035					1040
Ala	Pro	Val	Val	His	Val	Ser	Leu	Lys	Ser	Cys	Leu	Asp	Leu	Gly	Ile
				1045					1050					1055	
Thr	Ser	Tyr	Met	Thr	Thr	Pro	Cys	Lys	Leu	Ile	Asp	Leu	Gly	Asn	Gly
		1060						1065					1070		
Met	Ile	Pro	Ala	Leu	Glu	Asn	Arg	Ala	Thr	Pro	Ser	Leu	Ala	Asp	Asn
	1075					1080						1085			
Thr	Lys	Ser	Phe	Glu	Ile	Leu	Leu	Ala	Glu	Asp	Asn	Thr	Val	Asn	Gln
	1090					1095					1100				
Arg	Leu	Ala	Val	Lys	Ile	Leu	Glu	Lys	Tyr	His	His	Val	Val	Thr	Val
1105				1110						1115					1120
Val	Gly	Asn	Gly	Trp	Glu	Ala	Val	Lys	Ala	Val	Gln	Ser	Lys	Lys	Phe
				1125					1130					1135	
Asp	Val	Ile	Leu	Met	Asp	Val	Gln	Met	Pro	Ile	Met	Gly	Gly	Phe	Glu
		1140						1145					1150		
Ala	Thr	Gly	Lys	Ile	Arg	Glu	Tyr	Glu	Arg	Gly	Ile	Gly	Ser	His	Arg
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<210> 42
 <211> 3882
 <212> DNA
 <213> *Fusarium oxysporum*

<220>
 <221> CDS
 <222> (1)..(3882)

<400> 42
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 Met Val Asp Asp Ala Ala Leu Ala Ala Ser Ile Val Ala Ser
 1 5 10 15

att gct cca gat ccc cgt ctg ccc aat tcg ata ccg gtt ggt gta gct 96
 Ile Ala Pro Asp Pro Arg Leu Pro Asn Ser Ile Pro Val Gly Val Ala
 20 25 30

tct cag gtg caa ctc cca ggg cca gat act ccc gcc aag cgc aag ctc 144
 Ser Gln Val Gln Leu Pro Gly Pro Asp Thr Pro Ala Lys Arg Lys Leu
 35 40 45

gaa ctc gag ctt cag aac ctt gct cta cgt gtt gga aag ctc gag agc 192
 Glu Leu Glu Leu Gln Asn Leu Ala Leu Arg Val Gly Lys Leu Glu Ser
 50 55 60

cag gcc tca gct acc tct cca ttc cca gaa acg ccc aac gag gtt att 240
 Gln Ala Ser Ala Thr Ser Pro Phe Pro Glu Thr Pro Asn Glu Val Ile
 65 70 75 80

gac act ctt ttt ggc gaa gag gct cag gct gtg gcg gtc cgt ccc aag 288
 Asp Thr Leu Phe Gly Glu Glu Ala Gln Ala Val Ala Val Arg Pro Lys
 85 90 95

cct aaa gtc ttt cac gcc caa ggt agc ctg cac tct ccg cat ctg cca 336
 Pro Lys Val Phe His Ala Gln Gly Ser Leu His Ser Pro His Leu Pro
 100 105 110

tct tat cag ctg acc gaa gaa gcc ctt gaa gga ctt cga gaa cat gtg 384
 Ser Tyr Gln Leu Thr Glu Glu Ala Leu Glu Gly Leu Arg Glu His Val
 115 120 125

gac gac caa tcc aag tta ctc gat agt cag cgc cag gag ctc gct ggt 432
 Asp Asp Gln Ser Lys Leu Leu Asp Ser Gln Arg Gln Glu Leu Ala Gly
 130 135 140

gta aat gct cag ctc ttg gag cag aag cag cta caa gag cga gcc ctc 480
 Val Asn Ala Gln Leu Leu Glu Gln Lys Gln Leu Gln Glu Arg Ala Leu
 145 150 155 160

gag atc ctc gag cag gaa cgt att gct act ctg gag cgc gag ctt tgg 528
 Glu Ile Leu Glu Gln Glu Arg Ile Ala Thr Leu Glu Arg Glu Leu Trp
 165 170 175

aag cat cag aaa gcc aac gag gct ttc caa aag gct cta cga gaa att 576
 Lys His Gln Lys Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile
 180 185 190

gga gag att gtt aca gcc gtt gct cgc ggt gat ttg acc atg aag gtt 624
 Gly Glu Ile Val Thr Ala Val Ala Arg Gly Asp Leu Thr Met Lys Val
 195 200 205

cgc atg aac act gtt gaa atg gac cct gaa atc aca aca ttc aag cgc	672
Arg Met Asn Thr Val Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg	
210 215 220	
act atc aac gct atg atg gac cag ctg caa ata ttt gct agc gaa gtc	720
Thr Ile Asn Ala Met Met Asp Gln Leu Gln Ile Phe Ala Ser Glu Val	
225 230 235 240	
tcg cga gtc gct cgt gaa gtc ggt acc gaa gga ttg ctt ggt ggc caa	768
Ser Arg Val Ala Arg Glu Val Gly Thr Glu Gly Leu Leu Gly Gly Gln	
245 250 255	
gcc cgt atc ggc ggc gtc gac gga aca tgg aag gaa ttg act gac aac	816
Ala Arg Ile Gly Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn	
260 265 270	
gta aac gtt atg gcc cag aat ctt act gat caa gtg agg gag ata gca	864
Val Asn Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala	
275 280 285	
tcg gtt acc acc gcc gtg gcc cac ggc gat ctg act aaa aag atc gaa	912
Ser Val Thr Thr Ala Val Ala His Gly Asp Leu Thr Lys Lys Ile Glu	
290 295 300	
cga cct gcc aga ggc gag ata ttg caa tta caa caa acg att aac acc	960
Arg Pro Ala Arg Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr	
305 310 315 320	
atg gtg gac caa tta cga aca ttt gct tct gaa gtc aca cgt gta gcg	1008
Met Val Asp Gln Leu Arg Thr Phe Ala Ser Glu Val Thr Arg Val Ala	
325 330 335	
aga gat gtc ggg acc gaa ggc atg tta ggc ggg caa gcc gat gtt ggg	1056
Arg Asp Val Gly Thr Glu Gly Met Leu Gly Gly Gln Ala Asp Val Gly	
340 345 350	
gga gtg cag ggc atg tgg aac gat ctc acc gtc aat gtc aat gcc atg	1104
Gly Val Gln Gly Met Trp Asn Asp Leu Thr Val Asn Val Asn Ala Met	
355 360 365	
gcc aac aac ttg acg act caa gtg cgc gac att atc aag gtt acc aca	1152
Ala Asn Asn Leu Thr Thr Gln Val Arg Asp Ile Ile Lys Val Thr Thr	
370 375 380	
gct gtc gcc aag gga gat ctt aca caa aag gtc caa gcc gat tgc agg	1200
Ala Val Ala Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Asp Cys Arg	
385 390 395 400	
gga gag ata ttc gag ctc aag tca acc atc aac tcc atg gtt gac cag	1248
Gly Glu Ile Phe Glu Leu Lys Ser Thr Ile Asn Ser Met Val Asp Gln	
405 410 415	
ctg caa cag ttc gcc cgc gag gtt acc aag att gcc cgt gaa gtc gga	1296
Leu Gln Gln Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly	
420 425 430	
acc gaa gga cgc ctg gga ggg cag gcc act gtg cat gat gtt gaa ggc	1344
Thr Glu Gly Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Glu Gly	
435 440 445	

acc tgg agg gat ctg acg gag aac gtc aac ggc atg gcc atg aac ttg	1392
Thr Trp Arg Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu	
450 455 460	
acc act caa gtg cga gaa att gcc aag gtt aca aca gct gtc gcc aaa	1440
Thr Thr Gln Val Arg Glu Ile Ala Lys Val Thr Thr Ala Val Ala Lys	
465 470 475 480	
ggt gac ttg aca aag aag att ggg gtt gag gtc aag ggt gaa att gca	1488
Gly Asp Leu Thr Lys Lys Ile Gly Val Glu Val Lys Gly Glu Ile Ala	
485 490 495	
gaa ctg aag aac acc att aac cag atg gtg gat cgt ctt ggt acg ttt	1536
Glu Leu Lys Asn Thr Ile Asn Gln Met Val Asp Arg Leu Gly Thr Phe	
500 505 510	
gcc gtt gag gtg agc aag gta gcc agg gaa gta ggc aca gat gga aca	1584
Ala Val Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr	
515 520 525	
ttg ggt gga cag gct caa gtt gcc aat gtt gaa ggt aaa tgg aag gat	1632
Leu Gly Gly Gln Ala Gln Val Ala Asn Val Glu Gly Lys Trp Lys Asp	
530 535 540	
ctc aca gaa aac gtc aac aca atg gcg tca aat ctc aca gtc cag gtc	1680
Leu Thr Glu Asn Val Asn Thr Met Ala Ser Asn Leu Thr Val Gln Val	
545 550 555 560	
cga agt atc tca aca gtt act caa gcc att gcg aac ggc gac atg agc	1728
Arg Ser Ile Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser	
565 570 575	
cag aag atc aag gtc gaa gca aat gga gag ata caa gtg ctg aaa gaa	1776
Gln Lys Ile Lys Val Glu Ala Asn Gly Glu Ile Gln Val Leu Lys Glu	
580 585 590	
acc atc aat aac atg gtt gac cgt ttg tct agc ttc tgt tac gaa gtg	1824
Thr Ile Asn Asn Met Val Asp Arg Leu Ser Ser Phe Cys Tyr Glu Val	
595 600 605	
cag cga gtt gcc aag gat gtg ggt gtt gat gga aag atg ggt gct caa	1872
Gln Arg Val Ala Lys Asp Val Gly Val Asp Gly Lys Met Gly Ala Gln	
610 615 620	
gcc gac gta ggt ggt cta gac ggc cgc tgg aaa gag atc acc aca gat	1920
Ala Asp Val Gly Gly Leu Asp Gly Arg Trp Lys Glu Ile Thr Thr Asp	
625 630 635 640	
gtc aac aca atg gct agt aac ctg act aca caa gtg cgc gcc ttc tca	1968
Val Asn Thr Met Ala Ser Asn Leu Thr Thr Gln Val Arg Ala Phe Ser	
645 650 655	
gat ata acc aac ttg gcc acc gac ggg gat ttc acc aag cta gtc gac	2016
Asp Ile Thr Asn Leu Ala Thr Asp Gly Asp Phe Thr Lys Leu Val Asp	
660 665 670	
gtc gaa gca tcg ggt gag atg gac gag ctc aag cgc aag atc aac cag	2064
Val Glu Ala Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln	
675 680 685	

atg att tca aat ctg cgc gat tct att cag cgt aat act cag gcc agg	2112
Met Ile Ser Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Gln Ala Arg	
690 695 700	
 gaa gct gcc gaa ctt gcc aac aag acc aag tca gag ttc ctc gcc aac	2160
Glu Ala Ala Glu Leu Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn	
705 710 715 720	
 atg tcc cat gaa att cga acg ccg atg aac ggt atc atc gga atg act	2208
Met Ser His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr	
725 730 735	
 caa ctg aca ttg gac acc gat ctg act caa tat cag agg gag atg ctt	2256
Gln Leu Thr Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu	
740 745 750	
 aac att gtc aat aat ctt gcc aat agc ctc ttg acg ata att gac gat	2304
Asn Ile Val Asn Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp	
755 760 765	
 atc ttg gat ctt tcc aag att gaa gct cgg aga atg gtc att gag gag	2352
Ile Leu Asp Leu Ser Lys Ile Glu Ala Arg Arg Met Val Ile Glu Glu	
770 775 780	
 att cct tac aca ctg cgt gga acc gtc ttc aat gcc ctc aag act ctc	2400
Ile Pro Tyr Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu	
785 790 795 800	
 gct gtc aag gca aat gag aag ttc ttg gat ctc acc tac aag gtc gat	2448
Ala Val Lys Ala Asn Glu Lys Phe Leu Asp Leu Thr Tyr Lys Val Asp	
805 810 815	
 agc tcc gtg cct gac tac gtt att ggc gac tcc ttc cgt ctc aga caa	2496
Ser Ser Val Pro Asp Tyr Val Ile Gly Asp Ser Phe Arg Leu Arg Gln	
820 825 830	
 att atc ctc aac ctt gtt ggc aat gct atc aag ttc aca gag cat ggt	2544
Ile Ile Leu Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly	
835 840 845	
 gag gtc agc cta acg atc aag gag agc atg ggg caa aac aat gtc cga	2592
Glu Val Ser Leu Thr Ile Lys Glu Ser Met Gly Gln Asn Asn Val Arg	
850 855 860	
 cct gga gag tat gcg gtt gag ttt gtc gtg gag gac acg ggc ata gga	2640
Pro Gly Glu Tyr Ala Val Glu Phe Val Val Glu Asp Thr Gly Ile Gly	
865 870 875 880	
 atc gcc caa gat aaa ctg gat ttg atc ttc gac acg ttc caa caa gcg	2688
Ile Ala Gln Asp Lys Leu Asp Leu Ile Phe Asp Thr Phe Gln Gln Ala	
885 890 895	
 gat ggt tcc atg acg cgc aag ttt ggc gga aca ggt cta ggt cta tct	2736
Asp Gly Ser Met Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser	
900 905 910	
 att tcg aaa cga ctc gtc aat ctc atg ggt ggt gat ctc tgg gta aac	2784
Ile Ser Lys Arg Leu Val Asn Leu Met Gly Gly Asp Leu Trp Val Asn	
915 920 925	

agt gaa cat ggc aag ggc agt gaa ttt cac ttc aca tgc tta gtc aag	2832
Ser Glu His Gly Lys Gly Ser Glu Phe His Phe Thr Cys Leu Val Lys	
930 935 940	
ctt gct cct gac gat gct gct ctg atc gag caa cag atc cgc ccc tac	2880
Leu Ala Pro Asp Asp Ala Ala Leu Ile Glu Gln Gln Ile Arg Pro Tyr	
945 950 955 960	
cga ggt cat caa gtg cta ttc gtc gac aag gcc cag tcg cag aac gcc	2928
Arg Gly His Gln Val Leu Phe Val Asp Lys Ala Gln Ser Gln Asn Ala	
965 970 975	
acc tca atc aag cct atg ctt gag aag atc ggg ctg aag cct gtc gtt	2976
Thr Ser Ile Lys Pro Met Leu Glu Lys Ile Gly Leu Lys Pro Val Val	
980 985 990	
gtg gat tcg gag aag agt cct gcg ctg act cgt ctt caa agc ggt ggc	3024
Val Asp Ser Glu Lys Ser Pro Ala Leu Thr Arg Leu Gln Ser Gly Gly	
995 1000 1005	
tcc ctt ccc tat gat gct atc ctc gtc gat tcc atc gac act gcg aga	3072
Ser Leu Pro Tyr Asp Ala Ile Leu Val Asp Ser Ile Asp Thr Ala Arg	
1010 1015 1020	
agg tta aga gcc gtg gac gat ttc aag tac ctt cct atc gtc ttg ctg	3120
Arg Leu Arg Ala Val Asp Asp Phe Lys Tyr Leu Pro Ile Val Leu Leu	
1025 1030 1035 1040	
gca cca gtt gtt cac gtt agt ctg aag tcg tgc ttg gat ctg gga att	3168
Ala Pro Val Val His Val Ser Leu Lys Ser Cys Leu Asp Leu Gly Ile	
1045 1050 1055	
acg tcg tat atg acc acg cca tgc aag ctc att gat cta gga aat ggc	3216
Thr Ser Tyr Met Thr Thr Pro Cys Lys Leu Ile Asp Leu Gly Asn Gly	
1060 1065 1070	
atg att ccg gct ctc gag aac cgg gcg aca cct tca ctc gct gac aac	3264
Met Ile Pro Ala Leu Glu Asn Arg Ala Thr Pro Ser Leu Ala Asp Asn	
1075 1080 1085	
acg aaa tct ttc gaa att ctg ctc gcc gaa gac aac acc gtc aac caa	3312
Thr Lys Ser Phe Glu Ile Leu Leu Ala Glu Asp Asn Thr Val Asn Gln	
1090 1095 1100	
cga tta gca gtg aaa att ctc gag aag tat cac cat gtg gta aca gtg	3360
Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr Val	
1105 1110 1115 1120	
gtt ggt aac ggc tgg gaa gct gtc aaa gcc gtc caa agc aag aaa ttc	3408
Val Gly Asn Gly Trp Glu Ala Val Lys Ala Val Gln Ser Lys Lys Phe	
1125 1130 1135	
gat gtc att ctt atg gat gta caa atg ccg atc atg gga ggc ttc gaa	3456
Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly Gly Phe Glu	
1140 1145 1150	
gcc acg ggc aag att cga gaa tac gaa cgt ggc ata ggg agc cac cgc	3504
Ala Thr Gly Lys Ile Arg Glu Tyr Glu Arg Gly Ile Gly Ser His Arg	
1155 1160 1165	

aca ccc atc att gct cta acg gcc cac gcc atg atg ggt gac cga gag	3552
Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met Met Gly Asp Arg Glu	
1170 1175 1180	
aag tgt atc caa gct cag atg gac gag tat ttg tcc aaa ccc ttg cag	3600
Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Gln	
1185 1190 1195 1200	
caa aac cat ctc atc cag acg atc ctc aaa tgc gcg acg ctc ggc ggc	3648
Gln Asn His Leu Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly	
1205 1210 1215	
cct ttg ctt gaa aag aat cgt gaa cgg gaa ctg gca ctt cat gcc gag	3696
Pro Leu Leu Glu Lys Asn Arg Glu Arg Glu Leu Ala Leu His Ala Glu	
1220 1225 1230	
acg aaa tcg aag cac aag gag ggg gga cag ggt ctg cta cga ccc aca	3744
Thr Lys Ser Lys His Lys Glu Gly Gly Gln Gly Leu Leu Arg Pro Thr	
1235 1240 1245	
ctc gag agc cgc tca ttc aca agt cga gaa cct ctg ttg gga aat ggc	3792
Leu Glu Ser Arg Ser Phe Thr Ser Arg Glu Pro Leu Leu Gly Asn Gly	
1250 1255 1260	
aag gag agc cct gcc att ctg gct act gat gag gat ccc ctg gca aga	3840
Lys Glu Ser Pro Ala Ile Leu Ala Thr Asp Glu Asp Pro Leu Ala Arg	
1265 1270 1275 1280	
gca cgt ctt gac ctc tct gat atg cga agt ctt acc aac taa	3882
Ala Arg Leu Asp Leu Ser Asp Met Arg Ser Leu Thr Asn	
1285 1290	

<210> 43

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 43

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29

<210> 44

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 44

cgacaaggcc cagtcgcaga acgccacc

28

<210> 45
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 45
aagtttggcg gaacaggtct aggtctatc 29

<210> 46
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 46
tgccagcaag acgataggaa ggtacttga 29

<210> 47
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 47
cctcaccatg ctctgtgaac ttgatagc 28

<210> 48
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 48
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<210> 49
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 49
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<210> 50
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for DNA sequencing

<400> 50
 ccgaagacaa caccgtcaac caacgattag 30

<210> 51
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for DNA sequencing

<400> 51
 ggaccctgaa atcacaacat tcaagcgc 28

<210> 52
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for PCR

<400> 52
 tgcactagta tggttgacga cgcgggccctc gc 32

<210> 53
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for PCR

<400> 53
 gagctgcagt tagttggtaa gacttcgcat atc 33

<210> 54
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for DNA sequencing

<400> 54
 gtaaaacgac ggccag

16

<210> 55
 <211> 1307
 <212> PRT
 <213> Mycospharella tritici

<220>
 <221> misc_feature
 <222> (956)..(956)
 <223> Xaa is any amino acid

<220>
 <221> misc_feature
 <222> (1213)..(1213)
 <223> Xaa is any amino acid

<400> 55
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 1 5 10 15
 Phe Ala Lys Gln Tyr Ala Pro Leu Glu Ala Asp Ser Phe Pro Ala Lys
 20 25 30
 Ala Ile Ala Asn Gly Ile Lys Asn Thr Lys Ile Ala Leu Pro Gly Asp
 35 40 45
 Asp Ser Val Glu Lys Arg Thr Leu Glu Arg Glu Leu Thr Ser Leu Ala
 50 55 60
 Thr Arg Ile Gln Phe Leu Glu Ala Arg Ala Thr Ser Gly Thr Ser Ser
 65 70 75 80
 Leu Pro Ile Thr Pro Asn Glu Pro Leu Ser Ser Ala Phe Ser Glu Asp
 85 90 95
 Thr Ser Ser Pro Arg Ser Ala Ala Asn Gln His Arg Gln Arg Ser Ser
 100 105 110
 Ser Trp Val Asn Asn Leu Leu Ala Lys Ser Glu Gly Glu Pro His Pro
 115 120 125
 Arg Gln Leu Thr Glu Glu Gln Phe Ser Phe Leu Arg Glu His Ile Asp
 130 135 140
 Gln Gln Ala Gln Glu Ile Arg Thr Gln Lys Glu Phe Ile Asp Gly Ile
 145 150 155 160
 Lys Ser Gln Leu Thr His Gln Gln Thr Ala Thr Lys Ala Ala Leu Asp
 165 170 175
 Thr Leu Gly Asn Ser Gln Ser Ile Glu Gln Leu Lys Arg Glu Ile Glu
 180 185 190
 Lys Asn Ala Gln Ile Asn Ala Thr Tyr Gln Lys Val Leu Arg Glu Ile
 195 200 205
 Gly Thr Ile Ile Thr Ala Val Ala Asn Gly Asp Leu Ser Lys Lys Val
 210 215 220
 Leu Ile His Ala Thr Glu Lys Asp Pro Glu Ile Ala Arg Phe Lys His
 225 230 235 240
 Thr Ile Asn Lys Met Val Asp Gln Leu Gln Glu Phe Ala Ser Gln Val
 245 250 255
 Thr His Leu Ala Lys Glu Val Gly Thr Glu Gly Arg Leu Gly Gly Gln
 260 265 270
 Ala Val Val Pro Gly Val Asp Gly Ile Trp Ala Glu Leu Thr Gln Asn
 275 280 285

Val	Asn	Val	Met	Ala	Gln	Asn	Leu	Thr	Asp	Gln	Val	Arg	Glu	Ile	Ala		
	290					295					300						
Val	Val	Thr	Thr	Ala	Val	Ala	Gln	Gly	Asp	Leu	Ser	Arg	Lys	Ile	Gln		
305					310					315					320		
Arg	Pro	Ala	Arg	Gly	Glu	Ile	Leu	Gln	Leu	Gln	Gln	Thr	Ile	Asn	Ser		
				325					330					335			
Met	Val	Gly	Gln	Leu	Arg	Thr	Phe	Ala	Thr	Glu	Val	Thr	Arg	Val	Ser		
			340					345					350				
Arg	Asp	Val	Gly	Thr	Glu	Gly	Val	Leu	Gly	Gly	Gln	Ala	Gln	Ile	Glu		
		355					360					365					
Gly	Val	Gln	Gly	Met	Trp	Ser	Asp	Leu	Thr	Val	Asn	Val	Asn	Ala	Met		
	370					375					380						
Ala	Asn	Asn	Leu	Thr	Ala	Gln	Val	Arg	Asp	Ile	Ala	Glu	Val	Thr	Thr		
385					390					395					400		
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tct gat aat tcg agt ctt cct gca gat cac aat cgg ttg ctc acg ccc	3792
Ser Asp Asn Ser Ser Leu Pro Ala Asp His Asn Arg Leu Leu Thr Pro	
1250 1255 1260	
ccg aaa cga ccg ggt gtc gat cgt ggg tac acg gag aat gga ccg ccc	3840
Pro Lys Arg Pro Gly Val Asp Arg Gly Tyr Thr Glu Asn Gly Pro Pro	
1265 1270 1275 1280	
ggt ttg gaa agt ccg gcg ata gta acc gac gac cag gat gat ccg atg	3888
Gly Leu Glu Ser Pro Ala Ile Val Thr Asp Asp Gln Asp Asp Pro Met	
1285 1290 1295	
atc aga gag agt ctt gtt cgt gcc cat agc agc tga	3924
Ile Arg Glu Ser Leu Val Arg Ala His Ser Ser	
1300 1305	

<210> 57
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for PCR

 <400> 57
 cggaaggagt cgcccacgat gtagtcgg 28

 <210> 58
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for PCR

 <400> 58
 catggtggcg ccggccatct cggtgaac 28

 <210> 59
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for DNA sequencing

 <400> 59
 tcgccagacg cttcgacatt gatcatcttg 30

 <210> 60
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for DNA sequencing

 <400> 60
 ttcatggcca tgccatttac gttctccgtc 30

 <210> 61
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for DNA sequencing

<400> 61
 tacaagcgga accagttcgt tacccatcac 30

<210> 62
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for DNA sequencing

<400> 62
 gactccttcc gacttcgaca gatcattctc 30

<210> 63
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for DNA sequencing

<400> 63
 tccgtgtggt cgacccgtca gcctgctg 28

<210> 64
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for PCR

<400> 64
 cccactagta tgctgcaaga agagacttcg 30

<210> 65
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for PCR

<400> 65
 cctaagcttc tcagctgcta tgggcacgaa 30

<210> 66
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for DNA sequencing

<400> 66
 caggaaacag ctatgacat gattacgcca

30

<210> 67
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence : Designed
 oligonucleotide primer for DNA sequencing

<400> 67
 tgtaaaacga cggccagtga attgtaatac

30

<210> 68
 <211> 1438
 <212> PRT
 <213> Thanatephorus cucumeris

<400> 68
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 1 5 10 15
 Val Leu Ser Ile Tyr Glu Leu Gly Pro Gly Arg Pro Val Arg Ala Leu
 20 25 30
 Pro Thr Arg Ser Ser His Ser His Ser Ser Ser Gly Ser Arg His Ala
 35 40 45
 Arg Ala Leu Ser Val Pro Pro Phe Pro Pro Pro Pro Pro Met Ser Pro
 50 55 60
 Pro Asn Ala Pro Ile Asp Tyr Val Gly Ala Ala Pro Leu Pro Arg Tyr
 65 70 75 80
 Asp Gly Pro Arg Asp Trp Gln Thr Asp Ala Val Glu Arg Ala Leu Gly
 85 90 95
 Arg Val Ala Ala Arg Met Tyr Ala Ala Glu Ala Gln Leu Gln Asp Leu
 100 105 110
 Leu Ser Arg Glu Ser Ser Thr Ser Thr Pro Asp Pro Ala Leu Ser Pro
 115 120 125
 Arg Ser Asn Gly Leu Lys Lys Arg Arg Glu Asn Pro Gly Thr Pro Asp
 130 135 140
 Glu Arg Asp Pro Trp Gln Thr Val Arg Phe Gln Glu Val Gly Asp Gln
 145 150 155 160
 Asp Met Asp Pro Glu Pro Asp Thr Pro Val Ala Arg Pro Lys Asp Lys
 165 170 175
 Val Lys Pro Gly Thr Ile Asp Leu Ser Thr Leu Ser Gln Pro Thr Pro
 180 185 190
 Leu Ser Lys Val Ala Thr Asp Asn Pro Val Leu Pro Lys Pro Gly Pro
 195 200 205
 Arg Ser Ala Pro Thr Ser Ser Val Gly Ser Ile Met Pro Pro Phe Thr
 210 215 220
 Cys His Ser Cys Gly Arg Pro Met Gln Gly Pro Ala Ala Pro Asp Val
 225 230 235 240
 Ile His Ala Pro Gly Pro Leu Asp Val Val Thr Pro Ala Leu Gly Met
 245 250 255
 Gly Leu Gly Leu Ser Asp His Gly Ala Ala Glu Leu Arg Gln Lys Leu
 260 265 270

Gly	Phe	Gly	Asp	His	Glu	Asp	Asp	Thr	Gly	Ser	Pro	Leu	Val	Leu	Pro
		275					280					285			
Pro	Gly	Pro	Leu	Ser	Ala	Ala	Ala	Phe	Glu	Ser	Ala	Pro	Gly	Met	Ser
	290					295					300				
Ala	Val	Glu	Glu	Leu	Lys	Leu	Leu	Lys	Ala	Gln	Val	Gln	Asp	Val	Ala
305					310					315					320
Arg	Val	Cys	Lys	Ala	Val	Ala	Glu	Gly	Asp	Leu	Ser	Gln	Lys	Ile	Thr
				325					330					335	
Val	Pro	Val	Gln	Gly	Pro	Val	Met	Val	Gln	Leu	Lys	Asp	Val	Ile	Asn
			340					345					350		
Thr	Met	Val	Asp	Lys	Leu	Gly	Arg	Phe	Ala	Gln	Glu	Val	Thr	Arg	Val
		355					360					365			
Ser	Leu	Glu	Val	Gly	Thr	Glu	Gly	Arg	Leu	Gly	Gly	Gln	Ala	Ile	Val
	370					375					380				
Arg	Asp	Val	Arg	Gly	Thr	Trp	Ser	Glu	Leu	Thr	Thr	Val	Val	Asn	Arg
385					390					395					400
Leu	Ala	Ala	Asn	Leu	Thr	Ser	Gln	Val	Arg	Gly	Ile	Ala	Glu	Val	Thr
			405						410					415	
Lys	Ala	Val	Ala	Lys	Gly	Asp	Leu	Ser	Lys	Gln	Ile	Gly	Val	Asp	Ala
			420					425					430		
Lys	Gly	Glu	Ile	Leu	Glu	Leu	Lys	Asn	Thr	Val	Asn	Thr	Met	Val	Val
		435					440					445			
Arg	Leu	Arg	Met	Phe	Ala	Gly	Glu	Val	Thr	Arg	Val	Ala	Leu	Asp	Val
	450					455					460				
Gly	Ser	Arg	Gly	Ile	Leu	Gly	Gly	Gln	Ala	Tyr	Val	Pro	Asp	Val	Glu
465					470					475					480
Gly	Val	Trp	Gln	Glu	Leu	Thr	Asp	Asn	Val	Asn	Arg	Met	Cys	Ser	Asn
				485					490					495	
Leu	Thr	Asn	Gln	Val	Arg	Ser	Ile	Ala	Leu	Val	Thr	Thr	Ala	Val	Ala
			500					505					510		
Glu	Gly	Asp	Leu	Thr	Arg	Lys	Ile	Glu	Ile	Glu	Val	Glu	Gly	Glu	Met
		515					520					525			
Leu	Thr	Leu	Lys	Asn	Thr	Val	Asn	Ser	Met	Val	Asp	Gln	Leu	Ser	Thr
	530					535					540				
Phe	Ala	Ser	Glu	Val	Thr	Arg	Val	Ala	Leu	Glu	Val	Gly	Ser	Met	Gly
545					550					555					560
Ile	Leu	Gly	Gly	Gln	Ala	Gln	Val	Glu	Gly	Val	Lys	Gly	Thr	Trp	Ala
				565					570					575	
Asp	Leu	Thr	Arg	Asn	Val	Asn	Asn	Met	Ala	Ser	Asn	Leu	Thr	Asn	Gln
			580					585					590		
Val	Arg	Ser	Ile	Ala	Lys	Val	Thr	Thr	Ala	Val	Ala	His	Gly	Asp	Leu
		595					600					605			
Arg	Gln	Phe	Val	Glu	Val	Asp	Val	Gln	Gly	Glu	Met	Leu	Met	Leu	Lys
	610					615					620				
Asn	Thr	Val	Asn	Ser	Met	Val	Ala	Gln	Leu	Asp	Thr	Leu	Ala	Ser	Glu
625					630					635					640
Val	Ser	Arg	Val	Ala	Leu	Glu	Val	Gly	Ile	Glu	Gly	Arg	Leu	Gly	Gly
				645					650					655	
Gln	Ala	Val	Val	Gln	Gly	Val	Glu	Gly	Val	Trp	Lys	Val	Leu	Thr	Asp
			660					665					670		
Asn	Val	Asn	Leu	Met	Ala	Leu	Asn	Leu	Thr	Thr	Gln	Val	Arg	Ser	Ile
		675					680					685			
Ala	Ala	Val	Thr	Thr	Ala	Val	Ala	Arg	Gly	Asp	Leu	Ser	Lys	Asn	Ile
	690					695					700				
Asp	Val	Asp	Val	Lys	Gly	Glu	Ile	Leu	Asp	Leu	Lys	Ile	Thr	Val	Asn
705					710					715					720
Arg	Met	Thr	Asp	Ser	Leu	Arg	Ile	Phe	Ala	Ala	Glu	Val	Thr	Arg	Val
				725					730					735	
Ala	Arg	Glu	Val	Gly	Thr	Leu	Gly	Arg	Leu	Gly	Gly	Gln	Ala	Phe	Val
			740					745					750		

Pro	Gly	Val	Ala	Gly	Val	Trp	Lys	Asp	Leu	Thr	Asp	Asn	Val	Asn	Val		
		755					760					765					
Met	Ala	Ala	Asn	Leu	Thr	Leu	Gln	Val	Arg	Ala	Ile	Ala	Arg	Val	Thr		
		770					775					780					
Thr	Ala	Val	Ser	Val	Gly	Asp	Leu	Thr	Thr	Lys	Val	Glu	Gly	Ile	Asp		
785					790					795					800		
Val	Ala	Gly	Glu	Ile	Leu	Asp	Leu	Val	Asn	Thr	Ile	Asn	Gly	Met	Val		
				805					810					815			
Asp	Gln	Leu	Ala	Val	Phe	Ala	Ala	Glu	Val	Thr	Arg	Val	Ala	Arg	Glu		
			820					825					830				
Val	Gly	Thr	Glu	Gly	Arg	Leu	Gly	Val	Gln	Ala	Arg	Val	Glu	Gly	Met		
		835					840					845					
Gln	Gly	Ser	Trp	Gln	Ala	Ile	Thr	Val	Ser	Val	Asn	Thr	Met	Ala	Ala		
850					855						860						
Asn	Leu	Thr	Ser	Gln	Val	Arg	Gly	Phe	Ala	Gln	Ile	Ser	Ala	Ala	Ala		
865				870						875					880		
Thr	Asp	Gly	Asp	Phe	Thr	Arg	Phe	Ile	Thr	Val	Glu	Ala	Ser	Gly	Glu		
				885					890					895			
Met	Asp	Ser	Leu	Lys	Thr	Gln	Ile	Asn	Gln	Met	Val	Tyr	Asn	Leu	Arg		
		900						905					910				
Glu	Ser	Ile	Gln	Arg	Asn	Thr	Ala	Ala	Arg	Glu	Ala	Ala	Glu	Leu	Ala		
		915					920					925					
Asn	Arg	Ser	Lys	Ser	Glu	Phe	Leu	Ala	Asn	Met	Ser	His	Glu	Ile	Arg		
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Thr	Pro	Met	Asn	Gly	Ile	Ile	Gly	Met	Thr	Asp	Leu	Thr	Leu	Asp	Thr		
945				950						955					960		
Glu	Leu	Thr	Arg	Thr	Gln	Lys	Glu	Asn	Leu	Leu	Leu	Val	His	Gln	Leu		
				965					970					975			
Ala	Lys	Ser	Leu	Leu	Leu	Ile	Ile	Asp	Asp	Ile	Leu	Asp	Ile	Ser	Lys		
			980					985					990				
Ile	Glu	Ala	Gly	Arg	Met	Thr	Met	Glu	Gln	Val	Thr	Tyr	Ser	Leu	Arg		
		995				1000						1005					
Gly	Thr	Ala	Phe	Gly	Ile	Leu	Lys	Thr	Leu	Val	Val	Arg	Ala	His	Gln		
1010					1015						1020						
Gln	Asn	Leu	Asn	Leu	Phe	Tyr	Glu	Val	Asp	Pro	Glu	Ile	Pro	Asp	Gln		
1025				1030					1035					1040			
Val	Ile	Gly	Asp	Ser	Leu	Arg	Leu	Arg	Gln	Val	Ile	Thr	Asn	Leu	Val		
			1045					1050					1055				
Gly	Asn	Ala	Ile	Lys	Phe	Thr	Pro	Ser	Lys	Pro	Asn	Lys	Lys	Gly	Met		
		1060						1065				1070					
Val	Cys	Leu	Ser	Cys	Lys	Leu	Ile	Ser	Met	Asp	Glu	Gln	Asn	Val	Thr		
		1075				1080					1085						
Val	Arg	Phe	Cys	Val	Glu	Asp	Thr	Gly	Ile	Gly	Ile	Lys	Gln	Asp	Lys		
		1090			1095					1100							
Leu	Ala	Ile	Ile	Phe	Asp	Thr	Phe	Cys	Gln	Ala	Asp	Gly	Ser	Thr	Thr		
1105				1110					1115					1120			
Arg	Glu	Tyr	Gly	Gly	Thr	Gly	Leu	Gly	Leu	Ser	Ile	Ser	Lys	Arg	Leu		
			1125					1130				1135					
Val	Ser	Leu	Met	Asn	Gly	Gln	Met	Trp	Val	Glu	Ser	Glu	Val	Gly	Val		
		1140					1145					1150					
Gly	Ser	Arg	Phe	Tyr	Phe	Thr	Ile	Thr	Ala	Glu	Ile	Ser	Arg	Pro	Asn		
		1155				1160					1165						
Met	Ala	Gln	Ser	Leu	Gln	Lys	Val	Ala	Ile	Tyr	Lys	Glu	Arg	Thr	Ile		
		1170			1175						1180						
Leu	Phe	Val	Asp	Thr	Leu	Gly	Asp	Arg	Ser	Gly	Val	Ala	Glu	Arg	Ile		
1185				1190					1195					1200			
Glu	Glu	Leu	Gln	Leu	Arg	Pro	Phe	Val	Val	Arg	Asp	Ile	Ser	Gln	Val		
			1205					1210					1215				
Ala	Asp	Lys	Ala	Lys	Ile	Pro	Phe	Ile	Asp	Thr	Val	Ile	Val	Asp	Ser		
		1220					1225					1230					

Leu Glu Val Thr Glu Lys Leu Arg Glu Leu Asp His Leu Arg Tyr Thr
 1235 1240 1245
 Pro Ala Val Leu Leu Thr Pro Val Met Pro Arg Leu Asn Leu Thr Trp
 1250 1255 1260
 Cys Leu Glu Asn Phe Ile Ser Gly His Val Ala Thr Pro Ser Ser Leu
 1265 1270 1275 1280
 Asp Asp Leu Ala Glu Ala Leu Ala Lys Gly Leu Glu Ala Asn Ala Ser
 1285 1290 1295
 Gln Pro Glu Val Thr Pro Ser Asp Val Ala Tyr Asp Ile Leu Leu Ala
 1300 1305 1310
 Glu Asp Asn Val Val Asn Gln Arg Val Ala Val Lys Ile Leu Glu Lys
 1315 1320 1325
 Phe Gly His Thr Val Gln Ile Ala Glu Asn Gly Gln Phe Ala Val Asp
 1330 1335 1340
 Ala Val Lys Ala Arg Tyr Glu Gln Glu Lys Met Phe Asp Val Ile Leu
 1345 1350 1355 1360
 Met Asp Val Ser Met Pro Phe Met Gly Gly Met Glu Ala Thr Glu Ile
 1365 1370 1375
 Ile Arg Ala Phe Glu Lys Glu Lys Gly Ile Arg Arg Thr Pro Ile Ile
 1380 1385 1390
 Ala Leu Thr Ala His Ala Met Ile Gly Asp Arg Glu Arg Cys Ile Gln
 1395 1400 1405
 Ala Gly Met Asp Glu His Val Thr Lys Pro Leu Arg Arg Thr Asp Leu
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 Val Ser Ala Ile Lys Arg Leu Val Thr Pro His Gly Ala His
 1425 1430 1435

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 <212> DNA
 <213> *Thanatephorus cucumeris*

<220>
 <221> CDS
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 gtg ctg agt atc tat gag tta gga ccg gga cga cca gtg cgc gca ctg 96
 Val Leu Ser Ile Tyr Glu Leu Gly Pro Gly Arg Pro Val Arg Ala Leu
 20 25 30

 ccg acc cgg agc tca cat tcc cat tcc tct tcc ggt tcc cgc cat gcg 144
 Pro Thr Arg Ser Ser His Ser His Ser Ser Ser Gly Ser Arg His Ala
 35 40 45

 cgt gcg ctg tct gtg ccg ccg ttc cca cca ccg cca ccg atg tct ccg 192
 Arg Ala Leu Ser Val Pro Pro Phe Pro Pro Pro Pro Pro Met Ser Pro
 50 55 60

 ccg aac gca ccg atc gac tac gta ggc gct gct ccg ctg ccc cga tac 240
 Pro Asn Ala Pro Ile Asp Tyr Val Gly Ala Ala Pro Leu Pro Arg Tyr
 65 70 75 80

 gat gga ccg cgt gac tgg cag acg gat gcg gtc gag cga gca ctg ggc 288
 Asp Gly Pro Arg Asp Trp Gln Thr Asp Ala Val Glu Arg Ala Leu Gly
 85 90 95

cgt gtt gcc gcg cgg atg tac gcg gcc gag gcc cag ctg cag gac ctg	336
Arg Val Ala Ala Arg Met Tyr Ala Ala Glu Ala Gln Leu Gln Asp Leu	
100 105 110	
ctg agc cgc gag tcg agc aca tcc acc ccc gat ccc gct ctc tcg ccc	384
Leu Ser Arg Glu Ser Ser Thr Ser Thr Pro Asp Pro Ala Leu Ser Pro	
115 120 125	
cgc tcc aac ggc ctc aaa aaa cgc aga gag aac ccg gga aca ccc gat	432
Arg Ser Asn Gly Leu Lys Lys Arg Arg Glu Asn Pro Gly Thr Pro Asp	
130 135 140	
gag cgc gat ccg tgg cag act gtg cgc ttt caa gag gtc ggt gac cag	480
Glu Arg Asp Pro Trp Gln Thr Val Arg Phe Gln Glu Val Gly Asp Gln	
145 150 155 160	
gac atg gat ccc gag cca gac acc cct gtt gcc cgc ccc aag gac aag	528
Asp Met Asp Pro Glu Pro Asp Thr Pro Val Ala Arg Pro Lys Asp Lys	
165 170 175	
gtc aag cct ggt acc att gac ctg agt aca ctc tcc cag ccc act ccg	576
Val Lys Pro Gly Thr Ile Asp Leu Ser Thr Leu Ser Gln Pro Thr Pro	
180 185 190	
ctc tcc aag gtg gcc acg gac aat ccg gtg ctg ccc aag cct ggt ccc	624
Leu Ser Lys Val Ala Thr Asp Asn Pro Val Leu Pro Lys Pro Gly Pro	
195 200 205	
cgc agc gca ccc acc agc agc gtc gga tcc atc atg cct ccc ttc acg	672
Arg Ser Ala Pro Thr Ser Ser Val Gly Ser Ile Met Pro Pro Phe Thr	
210 215 220	
tgc cac tcg tgc gga cgc ccc atg cag ggc ccc gct gcc ccc gat gtc	720
Cys His Ser Cys Gly Arg Pro Met Gln Gly Pro Ala Ala Pro Asp Val	
225 230 235 240	
ata cac gca ccc ggt ccc ctc gac gtt gtc acc cct gca ctt ggc atg	768
Ile His Ala Pro Gly Pro Leu Asp Val Val Thr Pro Ala Leu Gly Met	
245 250 255	
ggc ctc ggt ctc tct gac cat ggc gct gcc gag ctc aga cag aaa ctt	816
Gly Leu Gly Leu Ser Asp His Gly Ala Ala Glu Leu Arg Gln Lys Leu	
260 265 270	
ggc ttt ggc gat cac gaa gac gac acc ggt agt ccc ctt gtt ctc ccc	864
Gly Phe Gly Asp His Glu Asp Asp Thr Gly Ser Pro Leu Val Leu Pro	
275 280 285	
cct ggc cct ctc agt gct gct gcc ttt gag agc gct cca ggc atg tcc	912
Pro Gly Pro Leu Ser Ala Ala Ala Phe Glu Ser Ala Pro Gly Met Ser	
290 295 300	
gcc gtc gaa gaa ctc aag ctg ctc aag gcc cag gtc cag gat gtc gct	960
Ala Val Glu Glu Leu Lys Leu Leu Lys Ala Gln Val Gln Asp Val Ala	
305 310 315 320	
cgt gta tgc aag gcc gtc gcc gag ggt gat ttg tct caa aag att acc	1008
Arg Val Cys Lys Ala Val Ala Glu Gly Asp Leu Ser Gln Lys Ile Thr	
325 330 335	

gtc	ccc	gtt	caa	ggg	ccc	gtc	atg	gtc	cag	ctc	aag	gat	gtc	atc	aac	1056
Val	Pro	Val	Gln	Gly	Pro	Val	Met	Val	Gln	Leu	Lys	Asp	Val	Ile	Asn	
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acc	atg	gtc	gat	aaa	cta	ggc	agg	ttt	gcg	cag	gag	gtc	act	cgt	gtc	1104
Thr	Met	Val	Asp	Lys	Leu	Gly	Arg	Phe	Ala	Gln	Glu	Val	Thr	Arg	Val	
		355					360					365				
tcg	ctc	gaa	gtc	gga	act	gaa	ggc	cgg	ctc	ggg	ggg	cag	gcc	att	gtt	1152
Ser	Leu	Glu	Val	Gly	Thr	Glu	Gly	Arg	Leu	Gly	Gly	Gln	Ala	Ile	Val	
	370					375					380					
cgc	gat	gtc	cgc	gga	aca	tgg	agc	gaa	ctc	aca	acc	gtc	gtc	aat	cgt	1200
Arg	Asp	Val	Arg	Gly	Thr	Trp	Ser	Glu	Leu	Thr	Thr	Val	Val	Asn	Arg	
385					390					395					400	
ctc	gcc	gct	aat	ctc	aca	agc	cag	gtc	cgg	gga	atc	gca	gaa	gtc	acc	1248
Leu	Ala	Ala	Asn	Leu	Thr	Ser	Gln	Val	Arg	Gly	Ile	Ala	Glu	Val	Thr	
			405					410						415		
aag	gca	gtc	gcc	aag	ggc	gat	ctc	tcc	aaa	caa	atc	ggc	gtc	gat	gca	1296
Lys	Ala	Val	Ala	Lys	Gly	Asp	Leu	Ser	Lys	Gln	Ile	Gly	Val	Asp	Ala	
		420					425						430			
aaa	ggg	gaa	ata	ttg	gaa	ttg	aag	aat	acg	gtt	aat	acc	atg	gtc	gtc	1344
Lys	Gly	Glu	Ile	Leu	Glu	Leu	Lys	Asn	Thr	Val	Asn	Thr	Met	Val	Val	
	435					440						445				
cgg	ttg	cgt	atg	ttt	gca	ggc	gaa	gtc	acc	cga	gtc	gcg	ctc	gat	gtc	1392
Arg	Leu	Arg	Met	Phe	Ala	Gly	Glu	Val	Thr	Arg	Val	Ala	Leu	Asp	Val	
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ggc	agt	cgt	ggg	att	cta	ggc	ggg	cag	gct	tat	gtc	ccg	gat	gtc	gag	1440
Gly	Ser	Arg	Gly	Ile	Leu	Gly	Gly	Gln	Ala	Tyr	Val	Pro	Asp	Val	Glu	
465					470			475							480	
ggg	gtt	tgg	caa	gag	ttg	acg	gat	aat	gta	aat	cgc	atg	tgc	tcc	aat	1488
Gly	Val	Trp	Gln	Glu	Leu	Thr	Asp	Asn	Val	Asn	Arg	Met	Cys	Ser	Asn	
			485					490						495		
ttg	acc	aac	caa	gtc	cgt	tcg	att	gcg	ctc	gtt	act	acc	gcc	gtc	gcc	1536
Leu	Thr	Asn	Gln	Val	Arg	Ser	Ile	Ala	Leu	Val	Thr	Thr	Ala	Val	Ala	
		500						505					510			
gag	ggg	gac	ctc	aca	cgt	aaa	atc	gaa	att	gaa	gtc	gag	ggc	gaa	atg	1584
Glu	Gly	Asp	Leu	Thr	Arg	Lys	Ile	Glu	Ile	Glu	Val	Glu	Gly	Glu	Met	
		515					520					525				
ttg	acg	ctc	aag	aat	acg	gta	aac	agc	atg	gtg	gac	cag	ctt	tcg	acg	1632
Leu	Thr	Leu	Lys	Asn	Thr	Val	Asn	Ser	Met	Val	Asp	Gln	Leu	Ser	Thr	
	530					535					540					
ttt	gcg	agc	gaa	gtc	acg	cgg	gtc	gcg	ctc	gag	gtt	ggc	tcg	atg	ggg	1680
Phe	Ala	Ser	Glu	Val	Thr	Arg	Val	Ala	Leu	Glu	Val	Gly	Ser	Met	Gly	
545					550					555					560	
ata	ctc	ggg	ggg	cag	gcg	cag	gtc	gag	ggg	gta	aaa	gga	act	tgg	gcc	1728
Ile	Leu	Gly	Gly	Gln	Ala	Gln	Val	Glu	Gly	Val	Lys	Gly	Thr	Trp	Ala	
				565					570					575		

gac	ttg	acg	agg	aat	gtg	aat	aat	atg	gcg	tcc	aat	cta	acc	aat	caa	1776
Asp	Leu	Thr	Arg	Asn	Val	Asn	Asn	Met	Ala	Ser	Asn	Leu	Thr	Asn	Gln	
			580					585					590			
gtc	cgt	tcg	atc	gcc	aag	gtc	acg	acg	gcc	gtc	gcg	cac	ggt	gac	ctg	1824
Val	Arg	Ser	Ile	Ala	Lys	Val	Thr	Thr	Ala	Val	Ala	His	Gly	Asp	Leu	
		595					600					605				
cgg	cag	ttt	gtc	gaa	gtc	gat	gtc	cag	gga	gag	atg	ctc	atg	ttg	aag	1872
Arg	Gln	Phe	Val	Glu	Val	Asp	Val	Gln	Gly	Glu	Met	Leu	Met	Leu	Lys	
	610					615					620					
aac	acg	gtg	aat	agc	atg	gtg	gct	cag	ctc	gat	acg	ctc	gcg	agc	gag	1920
Asn	Thr	Val	Asn	Ser	Met	Val	Ala	Gln	Leu	Asp	Thr	Leu	Ala	Ser	Glu	
625					630					635					640	
gtg	tcg	cgt	gtc	gcg	ctc	gag	gtc	ggt	atc	gag	ggt	cga	ctc	ggt	gga	1968
Val	Ser	Arg	Val	Ala	Leu	Glu	Val	Gly	Ile	Glu	Gly	Arg	Leu	Gly	Gly	
				645					650					655		
cag	gct	gtg	gtt	cag	ggt	gtg	gag	ggt	gtg	tgg	aag	gtt	tta	acg	gac	2016
Gln	Ala	Val	Val	Gln	Gly	Val	Glu	Gly	Val	Trp	Lys	Val	Leu	Thr	Asp	
			660					665					670			
aat	gtc	aac	ttg	atg	gct	ctg	aat	ctg	acg	acc	caa	gtg	cgg	tct	att	2064
Asn	Val	Asn	Leu	Met	Ala	Leu	Asn	Leu	Thr	Thr	Gln	Val	Arg	Ser	Ile	
		675					680					685				
gcg	gct	gtg	acg	act	gcc	gtg	gcg	cgt	ggt	gac	ctt	agc	aag	aat	atc	2112
Ala	Ala	Val	Thr	Thr	Ala	Val	Ala	Arg	Gly	Asp	Leu	Ser	Lys	Asn	Ile	
		690				695					700					
gat	gtc	gat	gtc	aag	ggc	gag	att	ttg	gat	ttg	aag	att	acg	gtc	aat	2160
Asp	Val	Asp	Val	Lys	Gly	Glu	Ile	Leu	Asp	Leu	Lys	Ile	Thr	Val	Asn	
705					710					715					720	
cgc	atg	acg	gat	agt	ttg	cgg	ata	ttc	gct	gct	gaa	gtg	act	cgt	gtc	2208
Arg	Met	Thr	Asp	Ser	Leu	Arg	Ile	Phe	Ala	Ala	Glu	Val	Thr	Arg	Val	
				725				730						735		
gcg	cgc	gag	gtc	ggt	acg	ctc	gga	cga	ctc	ggc	gga	cag	gcg	ttt	gtt	2256
Ala	Arg	Glu	Val	Gly	Thr	Leu	Gly	Arg	Leu	Gly	Gly	Gln	Ala	Phe	Val	
			740					745					750			
cct	ggt	gtg	gct	ggc	gtg	tgg	aag	gat	ttg	acg	gat	aat	gtg	aat	gtt	2304
Pro	Gly	Val	Ala	Gly	Val	Trp	Lys	Asp	Leu	Thr	Asp	Asn	Val	Asn	Val	
		755					760					765				
atg	gct	gcc	aat	ttg	acg	ttg	caa	gta	cga	gct	att	gcc	cga	gtc	aca	2352
Met	Ala	Ala	Asn	Leu	Thr	Leu	Gln	Val	Arg	Ala	Ile	Ala	Arg	Val	Thr	
	770					775					780					
acg	gcc	gtg	tcg	gtc	gga	gac	ttg	acg	acc	aag	gtc	gaa	ggc	atc	gat	2400
Thr	Ala	Val	Ser	Val	Gly	Asp	Leu	Thr	Thr	Lys	Val	Glu	Gly	Ile	Asp	
785					790					795					800	
gtc	gcg	ggt	gaa	atc	ttg	gat	ctc	gtc	aac	acg	atc	aac	gga	atg	gtg	2448
Val	Ala	Gly	Glu	Ile	Leu	Asp	Leu	Val	Asn	Thr	Ile	Asn	Gly	Met	Val	
				805					810					815		

gac cag ctc gcc gtg ttt gcg gcc gag gtc acg agg gtc gca cgc gaa	2496
Asp Gln Leu Ala Val Phe Ala Ala Glu Val Thr Arg Val Ala Arg Glu	
820 825 830	
gtc gga acc gag ggt cgg ttg ggt gtt cag gct cgc gtc gaa ggt atg	2544
Val Gly Thr Glu Gly Arg Leu Gly Val Gln Ala Arg Val Glu Gly Met	
835 840 845	
caa ggc agc tgg cag gcg att acc gta tct gta aac acg atg gct gcc	2592
Gln Gly Ser Trp Gln Ala Ile Thr Val Ser Val Asn Thr Met Ala Ala	
850 855 860	
aac ttg acg tcc caa gtg cgt ggg ttt gcg caa atc tcg gca gcg gcg	2640
Asn Leu Thr Ser Gln Val Arg Gly Phe Ala Gln Ile Ser Ala Ala Ala	
865 870 875 880	
acc gac gga gac ttt acg cgc ttc atc acg gtc gaa gcg agc gga gag	2688
Thr Asp Gly Asp Phe Thr Arg Phe Ile Thr Val Glu Ala Ser Gly Glu	
885 890 895	
atg gac tcg ctc aag acg cag atc aat cag atg gtg tac aac ctc cgg	2736
Met Asp Ser Leu Lys Thr Gln Ile Asn Gln Met Val Tyr Asn Leu Arg	
900 905 910	
gag agt att cag agg aac acg gct gcg cgt gag gct gct gag ctt gcg	2784
Glu Ser Ile Gln Arg Asn Thr Ala Ala Arg Glu Ala Ala Glu Leu Ala	
915 920 925	
aat cgg tcc aag tcc gag ttc ctt gcc aac atg tcg cac gag att cga	2832
Asn Arg Ser Lys Ser Glu Phe Leu Ala Asn Met Ser His Glu Ile Arg	
930 935 940	
acg ccg atg aac ggg att att ggc atg acg gat ctc acg ctt gat acc	2880
Thr Pro Met Asn Gly Ile Ile Gly Met Thr Asp Leu Thr Leu Asp Thr	
945 950 955 960	
gaa ctt aca cgg acg caa aaa gaa aac ttg ttg ctc gtt cac cag ctc	2928
Glu Leu Thr Arg Thr Gln Lys Glu Asn Leu Leu Leu Val His Gln Leu	
965 970 975	
gcc aag tct cta ttg ctt att atc gat gat att ctt gat att tcc aag	2976
Ala Lys Ser Leu Leu Leu Ile Ile Asp Asp Ile Leu Asp Ile Ser Lys	
980 985 990	
atc gag gct ggc agg atg acc atg gaa caa gtc acg tat tct ctc cgc	3024
Ile Glu Ala Gly Arg Met Thr Met Glu Gln Val Thr Tyr Ser Leu Arg	
995 1000 1005	
ggt act gca ttc ggt atc ctc aag acc ctt gtc gtc cgg gct cac caa	3072
Gly Thr Ala Phe Gly Ile Leu Lys Thr Leu Val Val Arg Ala His Gln	
1010 1015 1020	
caa aat ctc aac ctg ttc tac gaa gtc gat ccc gag att ccg gac caa	3120
Gln Asn Leu Asn Leu Phe Tyr Glu Val Asp Pro Glu Ile Pro Asp Gln	
1025 1030 1035 1040	
gtc att ggc gat tcg ctc cgt ctg cga caa gtc att acc aac ctc gtc	3168
Val Ile Gly Asp Ser Leu Arg Leu Arg Gln Val Ile Thr Asn Leu Val	
1045 1050 1055	

gga aac gct atc aag ttc act ccc agc aag ccc aac aaa aag ggc atg	3216
Gly Asn Ala Ile Lys Phe Thr Pro Ser Lys Pro Asn Lys Lys Gly Met	
1060 1065 1070	
gtc tgc ctc tcg tgc aag ctc atc tcg atg gac gag cag aat gtg acg	3264
Val Cys Leu Ser Cys Lys Leu Ile Ser Met Asp Glu Gln Asn Val Thr	
1075 1080 1085	
gtt cgg ttc tgt gtc gag gac acg ggt atc ggt atc aag cag gat aaa	3312
Val Arg Phe Cys Val Glu Asp Thr Gly Ile Gly Ile Lys Gln Asp Lys	
1090 1095 1100	
ctc gcg atc atc ttt gat acg ttc tgt caa gcc gat ggg tcc acg act	3360
Leu Ala Ile Ile Phe Asp Thr Phe Cys Gln Ala Asp Gly Ser Thr Thr	
1105 1110 1115 1120	
cgt gaa tac ggt ggt acc ggt ctc ggc ttg tcc atc tcg aaa cga ctc	3408
Arg Glu Tyr Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Arg Leu	
1125 1130 1135	
gtg tct ctg atg aat ggc caa atg tgg gtc gag tcc gag gtc gga gtc	3456
Val Ser Leu Met Asn Gly Gln Met Trp Val Glu Ser Glu Val Gly Val	
1140 1145 1150	
ggg tcc cgc ttc tac ttt acg atc acc gcc gaa atc tcc cgg ccg aac	3504
Gly Ser Arg Phe Tyr Phe Thr Ile Thr Ala Glu Ile Ser Arg Pro Asn	
1155 1160 1165	
atg gcg caa agt ctg caa aag gtc gcg atc tac aag gag cgc acg atc	3552
Met Ala Gln Ser Leu Gln Lys Val Ala Ile Tyr Lys Glu Arg Thr Ile	
1170 1175 1180	
ttg ttt gtc gat act ctg ggc gac cgg tcg ggt gtg gcg gag cgt atc	3600
Leu Phe Val Asp Thr Leu Gly Asp Arg Ser Gly Val Ala Glu Arg Ile	
1185 1190 1195 1200	
gaa gag ctg cag ctg cgt ccg ttt gtc gtg cgg gat atc agc cag gtg	3648
Glu Glu Leu Gln Leu Arg Pro Phe Val Val Arg Asp Ile Ser Gln Val	
1205 1210 1215	
gcg gac aag gcc aag att ccg ttt atc gat acg gtg att gtg gat tcg	3696
Ala Asp Lys Ala Lys Ile Pro Phe Ile Asp Thr Val Ile Val Asp Ser	
1220 1225 1230	
ctc gag gtg act gag aaa ttg cgc gag ttg gat cat ttg agg tat acc	3744
Leu Glu Val Thr Glu Lys Leu Arg Glu Leu Asp His Leu Arg Tyr Thr	
1235 1240 1245	
ccg gcc gtg ctc ttg acg cca gtt atg ccc cga ctg aat ctg acg tgg	3792
Pro Ala Val Leu Leu Thr Pro Val Met Pro Arg Leu Asn Leu Thr Trp	
1250 1255 1260	
tgt ctt gag aac ttt atc tcg ggt cat gtc gcg acc ccg tct tcg ctc	3840
Cys Leu Glu Asn Phe Ile Ser Gly His Val Ala Thr Pro Ser Ser Leu	
1265 1270 1275 1280	
gac gat ctt gcc gag gcg ctc gca aag gga ctg gaa gcc aac gca tct	3888
Asp Asp Leu Ala Glu Ala Leu Ala Lys Gly Leu Glu Ala Asn Ala Ser	
1285 1290 1295	

cag ccc gag gtt acg ccc agc gac gtt gcg tac gac att cta ctg gcc	3936
Gln Pro Glu Val Thr Pro Ser Asp Val Ala Tyr Asp Ile Leu Leu Ala	
1300 1305 1310	
 gaa gac aat gtt gtc aac caa cgt gtg gcc gtc aag att ctc gaa aag	3984
Glu Asp Asn Val Val Asn Gln Arg Val Ala Val Lys Ile Leu Glu Lys	
1315 1320 1325	
 ttt ggt cac acg gtt cag att gcc gag aat gga cag ttt gcg gtc gac	4032
Phe Gly His Thr Val Gln Ile Ala Glu Asn Gly Gln Phe Ala Val Asp	
1330 1335 1340	
 gct gtc aag gct cga tac gaa caa gag aag atg ttt gat gtc att ctt	4080
Ala Val Lys Ala Arg Tyr Glu Gln Glu Lys Met Phe Asp Val Ile Leu	
1345 1350 1355 1360	
 atg gac gtg tct atg ccg ttc atg ggt gga atg gag gca aca gaa att	4128
Met Asp Val Ser Met Pro Phe Met Gly Gly Met Glu Ala Thr Glu Ile	
1365 1370 1375	
 att cgc gcg ttt gag aag gaa aag ggc atc cgc gcg acg cct att atc	4176
Ile Arg Ala Phe Glu Lys Glu Lys Gly Ile Arg Arg Thr Pro Ile Ile	
1380 1385 1390	
 gct ctc aca gcg cac gcg atg att ggt gat cgt gag cgc tgt atc cag	4224
Ala Leu Thr Ala His Ala Met Ile Gly Asp Arg Glu Arg Cys Ile Gln	
1395 1400 1405	
 gct ggc atg gat gaa cac gtt acg aaa ccg ttg agg aga acc gat ctc	4272
Ala Gly Met Asp Glu His Val Thr Lys Pro Leu Arg Arg Thr Asp Leu	
1410 1415 1420	
 gtg agc gcg atc aaa cgc ctc gta aca ccc cac ggt gcc cac taa	4317
Val Ser Ala Ile Lys Arg Leu Val Thr Pro His Gly Ala His	
1425 1430 1435	

<210> 70
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

<400> 70	
cgaagtcgat cccgagattc cggacc	26

<210> 71
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

<400> 71	
cccgactccg acctcgact cgacccac	28

cag ccc gag gtt acg ccc agc gac gtt gcg tac gac att cta ctg gcc	3936
Gln Pro Glu Val Thr Pro Ser Asp Val Ala Tyr Asp Ile Leu Leu Ala	
1300 1305 1310	
 gaa gac aat gtt gtc aac caa cgt gtg gcc gtc aag att ctc gaa aag	3984
Glu Asp Asn Val Val Asn Gln Arg Val Ala Val Lys Ile Leu Glu Lys	
1315 1320 1325	
 ttt ggt cac acg gtt cag att gcc gag aat gga cag ttt gcg gtc gac	4032
Phe Gly His Thr Val Gln Ile Ala Glu Asn Gly Gln Phe Ala Val Asp	
1330 1335 1340	
 gct gtc aag gct cga tac gaa caa gag aag atg ttt gat gtc att ctt	4080
Ala Val Lys Ala Arg Tyr Glu Gln Glu Lys Met Phe Asp Val Ile Leu	
1345 1350 1355 1360	
 atg gac gtg tct atg ccg ttc atg ggt gga atg gag gca aca gaa att	4128
Met Asp Val Ser Met Pro Phe Met Gly Gly Met Glu Ala Thr Glu Ile	
1365 1370 1375	
 att cgc gcg ttt gag aag gaa aag ggc atc cgc cgc acg cct att atc	4176
Ile Arg Ala Phe Glu Lys Glu Lys Gly Ile Arg Arg Thr Pro Ile Ile	
1380 1385 1390	
 gct ctc aca gcg cac gcg atg att ggt gat cgt gag cgc tgt atc cag	4224
Ala Leu Thr Ala His Ala Met Ile Gly Asp Arg Glu Arg Cys Ile Gln	
1395 1400 1405	
 gct ggc atg gat gaa cac gtt acg aaa ccg ttg agg aga acc gat ctc	4272
Ala Gly Met Asp Glu His Val Thr Lys Pro Leu Arg Arg Thr Asp Leu	
1410 1415 1420	
 gtg agc gcg atc aaa cgc ctc gta aca ccc cac ggt gcc cac taa	4317
Val Ser Ala Ile Lys Arg Leu Val Thr Pro His Gly Ala His	
1425 1430 1435	

<210> 70

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 70

cgaagtcgat cccgagattc cggacc

26

<210> 71

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 71

cccgactccg acctcggact cgacccac

28

<210> 72
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

 <400> 72
 ggtgagcccg gacgacaagg gtcttgag 28

 <210> 73
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

 <400> 73
 attcgctcga ggtgactgag aa 22

 <210> 74
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR
 <400> 74
 ttacctcatc gctatctctt 20

 <210> 75
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

 <400> 75
 aaggtcgcga tctacaagga gc 22

 <210> 76
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

<400> 76
 atggacgtgt ctatgccgtt ca 22

<210> 77
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

<400> 77
 cttcgaccgt gatgaagcgc gta 23

<210> 78
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

<400> 78
 acgaagacga caccggtagt cc 22

<210> 79
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

<400> 79
 atcgcagaag tcaccaaggc agt 23

<210> 80
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

<400> 80
 gccaccgatg tctccgccga ac 22

<210> 81
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

<400> 81
 cttgctaagg`tcaccacgcg cca 23

<210> 82
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

<400> 82
 ttctaggtgg tcaggcttat gtcc 24

<210> 83
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

<400> 83
 ccagctgcag gacctgctga gc 22

<210> 84
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

<400> 84
 ctcaagaccc ttgtcgtccg ggctcacc 28

<210> 85
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

<400> 85
 ggaactagta tggcaggtac aacgggggga cacc 34

<210> 86
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

 <400> 86
 tgcaagcttt tagtgggcac cgtggggtgt tacg 34

 <210> 87
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

 <400> 87
 tttctgcaca atatttcaag ctatacc 27

 <210> 88
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

 <400> 88
 gacctagact tcagggtgtc taactcc 27

 <210> 89
 <211> 372
 <212> DNA
 <213> Phytophthora infestans

 <220>
 <221> CDS
 <222> (1)..(372)

 <400> 89
 cac gag att cgc aca ccc atg aat ggg att att ggc atg acg gat ctc 48
 His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Asp Leu
 1 5 10 15

 acg ctt gat acc gaa ctt aca cgg acg caa aaa gaa aac ttg ttg ctc 96
 Thr Leu Asp Thr Glu Leu Thr Arg Thr Gln Lys Glu Asn Leu Leu Leu
 20 25 30

 gtt cac cag ctc gcc aag tct cta ttg ctc att atc gat gat att ctt 144
 Val His Gln Leu Ala Lys Ser Leu Leu Leu Ile Ile Asp Asp Ile Leu
 35 40 45

gat att tcc aag atc gag gct ggc agg atg acc atg gaa caa gtc acg	192
Asp Ile Ser Lys Ile Glu Ala Gly Arg Met Thr Met Glu Gln Val Thr	
50 55 60	
tat tct ctc cgc ggc acc gca ttc ggt atc ctc aag acc ctt gtc gtc	240
Tyr Ser Leu Arg Gly Thr Ala Phe Gly Ile Leu Lys Thr Leu Val Val	
65 70 75 80	
cgg gct cac caa caa aat ctc aac ctg ttc tac gaa gtc gat ccc gag	288
Arg Ala His Gln Gln Asn Leu Asn Leu Phe Tyr Glu Val Asp Pro Glu	
85 90 95	
att ccg gac caa gtc att ggt gat tcg ctc cgt ctg cga caa gtc att	336
Ile Pro Asp Gln Val Ile Gly Asp Ser Leu Arg Leu Arg Gln Val Ile	
100 105 110	
acc aac ctc gtt gga aac gcc atc aag ttc aca gag	372
Thr Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu	
115 120	

<210> 90

<211> 124

<212> PRT

<213> Phytophthora infestans

<400> 90

His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Asp Leu	
1 5 10 15	
Thr Leu Asp Thr Glu Leu Thr Arg Thr Gln Lys Glu Asn Leu Leu Leu	
20 25 30	
Val His Gln Leu Ala Lys Ser Leu Leu Leu Ile Ile Asp Asp Ile Leu	
35 40 45	
Asp Ile Ser Lys Ile Glu Ala Gly Arg Met Thr Met Glu Gln Val Thr	
50 55 60	
Tyr Ser Leu Arg Gly Thr Ala Phe Gly Ile Leu Lys Thr Leu Val Val	
65 70 75 80	
Arg Ala His Gln Gln Asn Leu Asn Leu Phe Tyr Glu Val Asp Pro Glu	
85 90 95	
Ile Pro Asp Gln Val Ile Gly Asp Ser Leu Arg Leu Arg Gln Val Ile	
100 105 110	
Thr Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu	
115 120	